

Fig. 1

met ser lys asn thr
val ser ser ala arg phe arg lys val asp val asp
glu tyr asp glu asn lys phe val asp glu glu asp
gly gly asp gly gln ala gly pro asp glu gly glu
val asp ser cys leu arg gln gly asn met thr ala
ala leu gln ala ala leu lys asn pro pro ile asn
thr **arg** ser gln ala val lys asp arg ala gly ser
ile val leu lys val leu ile ser phe lys ala **gly**
asp ile glu lys ala val gln ser leu asp **arg** asn
gly val asp leu leu met lys tyr ile tyr lys gly
phe glu ser pro ser asp asn ser ser ala **val** leu
leu gln trp his glu lys ala leu ala ala gly gly
val gly ser ile val arg val leu thr ala arg lys
thr val

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LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 2A (1/3)

ggtctgtgtg tgcgtgcgtg cgagtgaagt agtgtgtgca tttttttttt tctctttttct	60
ttctctctct tttttttttt ttgtcaaaga aacagcagcg ccgccgcgcg tccgccgagg	120
cgctgcgccc cccggggggg ggaggcggag gaggcgggca gcggcggagg gaggggagcc	180
ggggaggggg gcgcgcgcgt gggagggagg cagcgcgcac ggtgcagccg ggccgggcgg	240
gaggc atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc	290
Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala	
1 5 10 15	
gcc acc acg gcc gcg gcc gcc gcc tgc tgc tcc gcc gct tcc ccg cac	338
Ala Thr Thr Ala Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His	
20 25 30	
tac caa gag tgg att ctg gac acc atc gac tgc ctg cgc tgc cgc aag	386
Tyr Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys	
35 40 45	
gcg cgg ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac	434
Ala Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His	
50 55 60	
ggc ccg gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag	482
Gly Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln	
65 70 75	
cag cgc gcc gtg ctc cgg gtc agc tac aag ggg agc atc tgc tac cgc	530
Gln Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg	
80 85 90 95	
aac gcg gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc	578
Asn Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala	
100 105 110	
ccg ccg cgc gcc ccc cgc ggg ggc ccc gcc gcc gcc gcc gcg ccg ccg	626
Pro Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg ccg ccg ccc gcg ccc gtc gcc gcc gcc gcc	674
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
gcc ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc gct gcc gcc aca	722
Ala Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Ala Ala Thr	
145 150 155	
gcg ccc ccc tgc ccc ggc ccc gcg cag ccg ggc ccc cgc gcg cag cgg	770
Ala Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg	
160 165 170 175	
gcc gcg ccc ctg gcc gcg ccg ccg ccc gcg ccc gcc gct ccc ccg gcg	818
Ala Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala	
180 185 190	

100 Years of Progress

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LEVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 2A (continued 2/3)

gcg gcg ccc ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gcc gcc	866
Ala Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala	
195 200 205	
gtc gcc gcc cgg gag tcg ccg ctg ccg ccg ccg cca cag ccg ccg gcg	914
Val Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala	
210 215 220	
ccg cca cag cag cag cag cag ccg ccg ccg cca ccg ccg ccg cag cag	962
Pro Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Gln	
225 230 235	
cca cag ccg ccg ccg gag ggg ggc gcg gcg cgg gcc ggc ggc ccg gcg	1010
Pro Gln Pro Pro Pro Glu Gly Gly Ala Ala Arg Ala Gly Gly Pro Ala	
240 245 250 255	
cgg ccc gtg agc ctg cgg gaa gtc gtg cgc tac ctc ggg ggt agc agc	1058
Arg Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser	
260 265 270	
ggc gct ggc ggc cgc ctg acc cgc ggc cgc gtg cag ggt ctg ctg gaa	1106
Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu	
275 280 285	
gag gag gcg gcg gcg cgg ggc cgc ctg gag cgc acc cgt ctc gga gcg	1154
Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala	
290 295 300	
ctt gcg ctg ccc cgc ggg gac agg ccc gga cgg gcg cca ccg gcc gcc	1202
Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala	
305 310 315	
agc gcc cgc gcg gcg cgg aac aag aga gct ggc gag gag cga gtg ctt	1250
Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu	
320 325 330 335	
gaa aag gag gag gag gag gag gag gag gaa gac gac gag gac gac gac	1298
Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp	
340 345 350	
gac gac gtc gtg tcc gag ggc tcg gag gtg ccc gag agc gat cgt ccc	1346
Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro	
355 360 365	
gcg ggt gcg cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg cag	1394
Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln	
370 375 380	
acc gcc aag gag cgg gcc aag gag tgg tcg ctg tgt ggc ccc cac cct	1442
Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro	
385 390 395	
ggc cag gag gaa ggg cgg ggg ccg gcc gcg ggc agt ggc acc cgc cag	1490
Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln	
400 405 410 415	

FOUO "SECRET"

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NEW LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 2A (continued 3/3)

gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg 1538
Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser
420 425 430

acc acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag 1586
Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys
435 440 445

cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg 1634
Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly
450 455 460

cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc 1682
Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val
465 470 475

gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc 1730
Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe
480 485 490 495

cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc 1778
Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr
500 505 510

gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc 1826
Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile
515 520 525

tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat 1874
Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp
530 535 540

gac ccg gaa ggc ttc ctg gga t gagcacagag ccgcccgcgcc ccttggtcccc 1926
Asp Pro Glu Gly Phe Leu Gly
545 550

acccccaccc cgccctggacc cattcctgcc tccatgtcac ccaaggtgtc ccagaggcca 1986
ggagctggac tgggcaggcg aggggtgcg acctaccctg attctggtag ggggcggggc 2046
cttgctgtgc tcattgctac cccccaccc cgtgtgtgtc tctgcacctg cccccagcac 2106
acccctcccg gagcctggat gtcgcctggg actctggcct gctcattttg cccccagatc 2166
agccccctcc ctccctcctg tcccaggaca ttttttaaaa gaaaaaaagg aaaaaaaaaa 2226
attggggagg gggctgggaa ggtgccccaa gatcctcctc ggcccaacca ggtgtttatt 2286
cctatatata tatatatatg ttttgttctg cctgtttttc gtttttttgt gcgtggcctt 2346
tcttccctcc caccaccact catggcccca gccctgctcg ccctgtcggc gggagcagct 2406
gggaatggga ggagggtggg accttggtgc tgtctccac cctctctccc gttggttctg 2466
ttgtcgctcc agctggctgt attgcttttt aatattgcac cgaagggttg tttttttttt 2526
tttaataaaa attttaaaaa aaggaaaaaa aaaaa 2561

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AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

fig. 2 B

asp cys arg ser ser ser asn asn arg Xaa pro lys
gly gly ala ala arg ala gly gly pro ala arg pro
val ser leu arg glu val val arg tyr leu gly gly
ser ser gly ala gly gly arg leu thr arg gly arg
val gln gly leu leu glu glu glu ala ala ala arg
gly arg leu glu arg thr arg leu gly ala leu ala
leu pro arg gly asp arg pro gly arg ala pro pro
ala ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp asp glu asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn **gly**
gly glu arg gly pro gln **thr** ala lys glu arg **ala**
lys glu trp **ser leu** cys gly pro his **pro** gly gln
glu glu gly arg gly pro ala **ala** gly ser gly thr
arg gln val phe ser met ala ala **leu ser** lys glu
gly gly **ser** ala ser **ser thr** thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro **ala** asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

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Fig. 3

ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp asp glu asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn gly
gly glu arg gly pro gln thr ala lys glu arg ala
lys glu trp ser leu cys gly pro his pro gly gln
glu glu gly arg gly pro ala ala gly ser gly thr
arg gln val phe ser met ala ala leu ser lys glu
gly gly ser ala ser ser thr thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro ala asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
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Fig. 4

thr arg leu gly ala leu ala
leu pro arg gly asp arg pro gly arg ala pro pro
ala ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp asp glu asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn gly
gly glu arg gly pro gln thr ala lys glu arg ala
lys glu trp ser leu cys gly pro his pro gly gln
glu glu gly arg gly pro ala ala gly ser gly thr
arg gln val phe ser met ala ala leu ser lys glu
gly gly ser ala ser ser thr thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro ala asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

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Fig. 5

met lys asn gln
asp lys lys asn gly ala ala lys gln pro asn pro
lys ser ser pro gly gln pro glu ala gly ala glu
gly ala gln gly arg pro gly arg pro ala pro ala
arg glu ala glu gly ala ser ser gln ala pro gly
arg pro glu gly ala gln ala lys thr ala gln pro
gly ala leu cys asp val ser glu glu leu ser arg
gln leu glu asp ile leu ser thr tyr cys val asp
asn asn gln gly ala pro gly glu asp gly val gln
gly glu pro pro glu pro glu asp ala glu lys ser
arg ala tyr val ala arg asn gly glu pro glu pro
gly thr pro val val asn gly glu lys glu thr ser
lys ala glu pro gly thr glu glu ile arg thr ser
asp glu val gly asp arg asp his arg arg pro gln
glu lys lys lys ala lys gly leu gly lys glu ile
thr leu leu met gln thr leu asn thr leu ser thr
pro glu glu lys leu ala ala leu cys lys lys tyr
ala glu leu leu glu glu his arg asn ser gln lys
gln met lys leu leu gln lys lys gln ser gln leu
val gln glu lys asp his leu arg gly glu his ser
lys ala ile leu ala arg ser lys leu glu ser leu
cys arg glu leu gln arg his asn arg ser leu lys
glu glu gly val gln arg ala arg glu glu glu glu
lys arg lys glu val thr ser his phe gln met thr
leu asn asp ile gln leu gln met glu gln his asn
glu arg asn ser lys leu arg gln glu asn met glu

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 5 (continued)

leu ala glu arg leu lys lys leu ile glu gln tyr
glu leu arg glu glu his ile asp lys val phe lys
his lys asp leu gln gln gln leu val asp ala lys
leu gln gln ala gln glu met leu lys glu ala glu
glu arg his gln arg glu lys asp phe leu leu lys
glu ala val glu ser gln arg met cys glu leu met
lys gln gln glu thr his leu lys gln gln leu ala
leu tyr thr glu lys phe glu glu phe gln asn thr
leu ser lys ser ser glu val phe thr thr phe lys
gln glu met glu lys met thr lys lys ile lys lys
leu glu lys glu thr thr met tyr arg ser arg trp
glu ser ser asn lys ala leu leu glu met ala glu
glu lys thr leu arg asp lys glu leu glu gly leu
gln val lys ile gln arg leu glu lys leu cys arg
ala leu gln thr glu arg asn asp leu asn lys arg
val gln asp leu ser ala gly gly gln gly **pro val**
ser asp ser gly pro glu arg arg pro **glu pro ala**
thr thr ser lys glu gln gly val glu gly pro gly
ala gln **val** pro **asn** ser pro arg **ala thr asp ala**
ser cys **cys ala** gly ala pro ser thr glu ala ser
gly gln thr gly pro gln glu pro thr **thr ala thr**
ala

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Fig. 6

met ser lys asn thr val ser ser ala
arg phe arg lys val asp val asp glu tyr asp glu
asn lys phe val asp glu glu asp gly gly asp gly
gln ala gly pro asp glu gly glu val asp ser cys
leu arg gln gly asn met thr ala ala leu gln ala
ala leu lys asn pro pro ile asn thr **lys** ser gln
ala val lys asp arg ala gly ser ile val leu lys
val leu ile ser phe lys ala **asn** asp ile glu lys
ala val gln ser leu asp **lys** asn gly val asp leu
leu met lys tyr ile tyr lys gly phe glu ser pro
ser asp asn ser ser ala **met** leu leu gln trp his
glu lys ala leu ala ala gly gly val gly ser ile
val arg val leu thr ala arg lys thr val

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LEVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 7A (1/3)

atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcc gcc	48
Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala Ala	
1 5 10 15	
acc acg gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa	96
Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His Tyr Gln	
20 25 30	
gag tgg atc ctg gac acc atc gac tcg ctg cgc tcg cgc aag gcg ccg	144
Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg	
35 40 45	
ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac gcc ccg	192
Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro	
50 55 60	
gag ccg gag cgc acg cgc gcc gag ctg gag aaa ctg atc cag cag cgc	240
Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg	
65 70 75 80	
gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc aac gcg	288
Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala	
85 90 95	
gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc ccg ccg	336
Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro	
100 105 110	
cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcc gcc ccg ccg	384
Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc	432
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc gcc aca gcg ccc ccc	480
Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Thr Ala Pro Pro	
145 150 155 160	
tcg cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg gcc gcg ccc	528
Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro	
165 170 175	
ctg gcc gcg ccg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc	576
Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro	
180 185 190	
ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc ccg gag	624
Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu	
195 200 205	
ccg ccg ctg ccg ccg ccg cca cag ccg ccg gcg ccg cca cag cag cag	672
Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln	
210 215 220	

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MODEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 7A (continued; 2/3)

cag ccg ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg gtg	720
Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val	
225 230 235 240	
cgg gcc ggc ggc gcg gcg ccg ccc gtg agc ctg ccg gaa gtc gtg cgc	768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg	
245 250 255	
tac ctc ggg ggc agc ggc ggc gcc gcc ggt cgc cta acc cgc ggc cgc	816
Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg	
260 265 270	
gtg cag ggg ctg ctg gag gag gag gcg gcg gct cga ggc cgt ctg gag	864
Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu	
275 280 285	
cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga	912
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly	
290 295 300	
cgg gcg ccg ccg gcc gcc agc gcc cgc ccg tct cgc agc aag aga ggt	960
Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly	
305 310 315 320	
gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa	1008
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu	
325 330 335	
gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag	1056
Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu	
340 345 350	
agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag ccg	1104
Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg	
355 360 365	
gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga	1152
Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly	
370 375 380	
ccg cac cag ggc cag gat gaa ggg ccg ggg cca gcc ccg ggc agc gcc	1200
Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly	
385 390 395 400	
acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca	1248
Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr	
405 410 415	
gct tct gtt gcc acc ggg cca gac tcc ccg tcc ccc gtg cct ttg ccc	1296
Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro	
420 425 430	
cca gcc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt	1344
Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys	
435 440 445	

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LEVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
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 ATHEROSCLEROSIS

Fig. 7A (continued; 3/3)

ccg ccc ggg cgc aaa gag aag cca tct gat ccc gtc gag tgg acc gtg	1392
Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val	
450 455 460	
atg gat gtc gtc gaa tat ttt act gag gct gga ttc ccg gag cag gcg	1440
Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala	
465 470 475 480	
aca gct ttc caa gag cag gaa att gat ggc aaa tct ttg ctg ctc atg	1488
Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met	
485 490 495	
cag cgc aca gat gtg ctc acc ggc ctg tcc atc cgc ctc ggg cca gcc	1536
Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala	
500 505 510	
ctg aaa atc tac gag cac cac atc aag gtg ctt cag caa ggc cac ttt	1584
Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe	
515 520 525	
gag gat gat gac ccc gat ggc ttc tta ggc	1614
Glu Asp Asp Asp Pro Asp Gly Phe Leu Gly	
530 535	

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 7B

glu glu arg val leu glu lys glu glu glu glu asp
asp asp glu asp glu asp glu glu asp asp val ser
glu gly ser glu val pro glu ser asp arg pro ala
gly ala gln his his gln leu asn gly glu arg gly
pro gln ser ala lys glu arg val lys glu trp thr
pro cys gly pro his gln gly gln asp glu gly arg
gly pro ala pro gly ser gly thr arg gln val phe
ser met ala ala met asn lys glu gly gly thr ala
ser val ala thr gly pro asp ser pro ser pro val
pro leu pro pro gly lys pro ala leu pro gly ala
asp gly thr pro phe gly cys pro pro gly arg lys
glu lys pro ser asp pro val glu trp thr val met
asp val val glu tyr phe thr glu ala gly phe pro
glu gln ala thr ala phe gln glu gln glu ile asp
gly lys ser leu leu leu met gln arg thr asp val
leu thr gly leu ser ile arg leu gly pro ala leu
lys ile tyr glu his his ile lys val leu gln gln
gly his phe glu asp asp asp pro asp gly phe leu
gly

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 8A (1/3)

atg Met 1	aag Lys	aac Asn	caa Gln	gac Asp 5	aaa Lys	aag Lys	aac Asn	ggg Gly	ggt Ala 10	gcc Ala	aaa Lys	caa Gln	tcc Ser	aat Asn 15	cca Pro	48
aaa Lys	agc Ser	agc Ser	cca Pro 20	gga Gly	caa Gln	ccg Pro	gaa Glu	gca Ala 25	gga Gly	ccc Pro	gag Glu	gga Gly	gcc Ala 30	cag Gln	gag Glu	96
cgg Arg	ccc Pro	agc Ser 35	cag Gln	gcg Ala	gct Ala	cct Pro	gca Ala 40	gta Val	gaa Glu	gca Ala	gaa Glu	ggt Gly 45	ccc Pro	ggc Gly	agc Ser	144
agc Ser	cag Gln 50	gct Ala	cct Pro	cgg Arg	aag Lys	ccg Pro 55	gag Glu	ggt Gly	gct Ala	caa Gln	gcc Ala 60	aga Arg	acg Thr	gct Ala	cag Gln	192
tct Ser 65	ggg Gly	gcc Ala	ctt Leu	cgt Arg	gat Asp 70	gtc Val	tct Ser	gag Glu	gag Glu	ctg Leu 75	agc Ser	cgc Arg	caa Gln	ctg Leu 80	gaa Glu	240
gac Asp	ata Ile	ctg Leu	agc Ser	aca Thr 85	tac Tyr	tgt Cys	gtg Val	gac Asp	aat Asn 90	aac Asn	cag Gln	ggg Gly	ggc Gly	ccc Pro 95	ggc Gly	288
gag Glu	gat Asp	ggg Gly	gca Ala 100	cag Gln	ggt Gly	gag Glu	ccg Pro	gct Ala 105	gaa Glu	ccc Pro	gaa Glu	gat Asp	gca Ala 110	gag Glu	aag Lys	336
tcc Ser	cgg Arg	acc Thr 115	tat Tyr	gtg Val	gca Ala	agg Arg	aat Asn 120	ggg Gly	gag Glu	cct Pro	gaa Glu	cca Pro 125	act Thr	cca Pro	gta Val	384
gtc Val 130	aat Asn	gga Gly	gag Glu	aag Lys	gaa Glu	ccc Pro 135	tcc Ser	aag Lys	ggg Gly	gat Asp	cca Pro 140	aac Asn	aca Thr	gaa Glu	gag Glu	432
atc Ile 145	cgg Arg	cag Gln	agt Ser	gac Asp 150	gag Glu	gtc Val	gga Gly	gac Asp	cga Arg	gac Asp 155	cat His	cga Arg	agg Arg	cca Pro	cag Gln 160	480
gag Glu	aag Lys	aaa Lys	aaa Lys	gcc Ala 165	aag Lys	ggt Gly	ttg Leu	ggt Gly	aag Lys	gag Glu	atc Ile	acg Thr	ttg Leu	ctg Leu	atg Met	528
cag Gln	aca Thr	ttg Leu	aat Asn	act Thr	ctg Leu	agt Ser	acc Thr	cca Pro	gag Glu	gag Glu	aag Lys	ctg Leu	gct Ala	gct Ala	ctg Leu	576
tgc Cys	aag Lys	aag Lys	tat Tyr	gct Ala	gaa Glu	ctg Leu	ctg Leu	gag Glu	gag Glu	cac His	cgg Arg	aat Asn	tca Ser	cag Gln	aag Lys	624

[illegible]

Applicant(s): Ann M. Lees et al.

LOW DENSITY LIPOPROTEIN BINDING PROTEINS
 AND THEIR USE IN DIAGNOSING AND TREATING
 ATHEROSCLEROSIS

Fig. 8A (continued; 2/3)

cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag aag Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys 210 215 220	672
gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc aag Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys 225 230 235 240	720
ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc aag Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys 245 250 255	768
gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag gag Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys Glu 260 265 270	816
gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag atg Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met 275 280 285	864
gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg gag Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu 290 295 300	912
ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc gag Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu 305 310 315 320	960
gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag ctg Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu 325 330 335	1008
gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca gaa Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu 340 345 350	1056
gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta gag Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu 355 360 365	1104
tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg aag Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys 370 375 380	1152
caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac aca Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr 385 390 395 400	1200
ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg gaa Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu 405 410 415	1248

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 8A (continued; 3/3)

aag Lys	atg Met	act Thr	aag Lys	aag Lys	atc Ile	aag Lys	aag Lys	ctg Leu	gag Glu	aaa Lys	gaa Glu	acc Thr	acc Thr	atg Met	tac Tyr	1296
			420					425					430			
cgg Arg	tcc Ser	cgg Arg	tgg Trp	gag Glu	agc Ser	agc Ser	aac Asn	aag Lys	gcc Ala	ctg Leu	ctt Leu	gag Glu	atg Met	gct Ala	gag Glu	1344
			435					440					445			
gag Glu	aaa Lys	aca Thr	gtc Val	cgg Arg	gat Asp	aaa Lys	gaa Glu	ctg Leu	gag Glu	ggc Gly	ctg Leu	cag Gln	gta Val	aaa Lys	atc Ile	1392
			450					455					460			
caa Gln	cgg Arg	ctg Leu	gag Glu	aag Lys	ctg Leu	tgc Cys	cgg Arg	gca Ala	ctg Leu	cag Gln	aca Thr	gag Glu	cgc Arg	aat Asn	gac Asp	1440
			465					470					475		480	
ctg Leu	aac Asn	aag Lys	agg Arg	gta Val	cag Gln	gac Asp	ctg Leu	agt Ser	gct Ala	ggc Gly	ggc Gly	cag Gln	ggc Gly	tcc Ser	ctc Leu	1488
			485					490					495			
act Thr	gac Asp	agt Ser	ggc Gly	cct Pro	gag Glu	agg Arg	agg Arg	cca Pro	gag Glu	ggg Gly	cct Pro	ggg Gly	gct Ala	caa Gln	gca Ala	1536
			500					505					510			
ccc Pro	agc Ser	tcc Ser	ccc Pro	agg Arg	gtc Val	aca Thr	gaa Glu	gcg Ala	cct Pro	tgc Cys	tac Tyr	cca Pro	gga Gly	gca Ala	ccg Pro	1584
			515					520					525			
agc Ser	aca Thr	gaa Glu	gca Ala	tca Ser	ggc Gly	cag Gln	act Thr	ggg Gly	cct Pro	caa Gln	gag Glu	ccc Pro	acc Thr	tcc Ser	gcc Ala	1632
			530					535					540			
agg Arg	gcc Ala															1638
			545													

[illegible]

Fig. 8 B

lys ser ser pro gly gln pro glu ala gly pro glu gly ala
gln glu arg pro ser gln ala ala pro ala val glu ala glu gly
pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala
arg thr ala gln ser gly ala leu arg asp val ser glu glu leu
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn
asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala
glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn
gly glu pro glu pro thr pro val val tyr gly glu lys glu pro
ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu
val gly asp arg asp his arg arg pro gln glu lys lys lys ala
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met
lys leu leu gln lys lys gln ser gln leu val gln glu lys asp
his leu arg gly glu his ser lys ala val leu ala arg ser lys
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg
lys glu val thr ser his phe gln val thr leu asn asp ile gln
leu gln met glu gln his asn glu arg asn ser lys leu arg gln
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln
tyr glu leu arg glu glu his ile asp lys val phe lys his lys
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln
glu met leu lys glu ala glu glu arg his gln arg glu lys asp
phe leu leu lys glu ala val glu ser gln arg met cys glu leu
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

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Fig. 8 B(continued)

glu val phe thr thr phe lys gln glu met glu lys met thr lys
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys
thr val arg asp lys glu leu glu gly leu gln val lys ile gln
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala
gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu
pro thr ser ala arg ala ***

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Fig. 9

val asp val asp

glu tyr asp glu asn lys phe val asp glu glu asp

gly gly asp gly

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Fig. 10

1 AAG CCT CGC AGC GGT CGG GGC GGC GCC GCG GAG GCT
37 CGA GGG CGG CGG GCG GCG GCG ATG TCG AAG AAC ACG
met ser lys asn thr

73 GTG TCG TCG GCG CGG TTC CGG AAG GTG GAC GTG GAT
val ser ser ala arg phe arg lys val asp val asp

109 GAG TAC GAC GAG AAC AAG TTC GTG GAC GAG GAA GAC
glu tyr asp glu asn lys phe val asp glu glu asp

145 GGC GGC GAC GGC CAG GCG GGG CCG GAC GAG GGC GAG
gly gly asp gly gln ala gly pro asp glu gly glu

181 GTG GAC TCG TGC CTG CGG CAA GGG AAC ATG ACA GCC
val asp ser cys leu arg gln gly asn met thr ala

217 GCC CTG CAG GCG GCG CTG AAG AAC CCT CCC ATC AAC
ala leu gln ala ala leu lys asn pro pro ile asn

253 ACC AGG AGC CAG GCG GTG AAG GAC CGG GCA GGC AGC
thr **arg** ser gln ala val lys asp arg ala gly ser

289 ATC GTG CTG AAG GTG CTC ATC TCC TTC AAG GCC GGC
ile val leu lys val leu ile ser phe lys ala **gly**

325 GAC ATA GAA AAG GCC GTG CAG TCC CTG GAC AGG AAC
asp ile glu lys ala val gln ser leu asp **arg** asn

361 GGC GTG GAC CTG CTC ATG AAG TAC ATC TAC AAG GGC
gly val asp leu leu met lys tyr ile tyr lys gly

397 TTC GAG AGC CCC TCC GAC AAC AGC AGC GCC GTG CTC
phe glu ser pro ser asp asn ser ser ala **val** leu

433 CTG CAG TGG CAC GAG AAG GCG CTG GCT GCA GGA GGA
leu gln trp his glu lys ala leu ala ala gly gly

469 GTG GGC TCC ATC GTC CGT GTC CTG ACT GCA AGG AAA
val gly ser ile val arg val leu thr ala arg lys

505 ACC GTG TAG CCT GGC AGG AAC GGG TGC CTG CCG GGG
thr val

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
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ATHEROSCLEROSIS

Fig. 10 (continued)

541 AGC GGG AGC TGC CGG TAC AAA GAC CAA AAC GCC CAG
577 ATG CCG CCG CTG CCC TGT GGG CGG CGT CTG TTC CCA
613 GCT TCG CTT TTT CCC TTT CCC GTG TCT GTC AGG ATT
649 ACA TAA GGT TTC CCT TCG TGA GAA TCG GAG TGG CGC
685 AGA GGG TCC TGT TCA TAC GCG CCG TGC GTC CGG CTG
721 TGT AAG ACC CCT GCC TTC AGT GTC CTT GAG CAA CGG
757 TAG CGT GTC GCC GGC TGG GTT TGG TTT TGT CGT GGA
793 GGG ATC TGG TCA GAA TTT GAG GCC AGT TTC CTA ACT
829 CAT TGC TGG TCA GGA AAT GAT CTT CAT TTA AAA AAA
865 AAA AAA AGA CTG GCA GCT ATT ATG CAA AAC TGG ACC
901 CTC TTC CCT TAT TTA AGC AGA GTG AGT TTC TGG AAC
937 CAG TGG TGC CCC CCC CCC CGC CCC GGC CGC CGT CCT
973 GCT CAA GGG AAG CCT CCC TGC AGA GCA GCA GAG CCC
1009 CTG GGC AGG AGC GCC GCG TCC CGC TCC CAG GAG ACA
1045 GCA TGC GCG GTC ACG CGG CAC TTC CTG TGC CTC CCA
1081 GCC CCA GTG CCC CGG AGT TCT TCA GGG CGA CAG GGA
1117 CCT CAG AAG ACT GGA TCC GAT CCA GAC AGA CGC CCA
1153 TTC TTG GTT CAG CTC AGT GTT TTC AAA AGG AAC GTG
1189 CTA CCG TGG GTA GAG CAC ACT GGT TCT CAG AAC ACG
1225 GCC GGC GCT TGA CGG TTG TCA CAG CTC CAG AAC AAA
1261 TCC TGG GAG ACA GGC GAG CGC GAG TCG CCG GGC AGG
1297 AAT TCC ACA CAC TCG TGC TGT TTT TGA TAC CTG CTT
1333 TTT GTT TTG TTT TGT AAA AAT GAT GCA CTT GAG AAA
1369 ATA AAA CGT CAG TGT TGA CAA AAA AAA AAA AAA AAA

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Fig. 11

1 GAC TGC CGC AGC AGC AGC AAC AAC CGC TAG CCG AAG
asp cys arg ser ser ser asn asn arg Xaa pro lys

37 GGT GGC GCG GCG CGG GCC GGC GGC CCG GCG CGG CCC
gly gly ala ala arg ala gly gly pro ala arg pro

73 GTG AGC CTG CGG GAA GTC GTG CGC TAC CTC GGG GGT
val ser leu arg glu val val arg tyr leu gly gly

109 AGC AGC GGC GCT GGC GGC CGC CTG ACC CGC GGC CGC
ser ser gly ala gly gly arg leu thr arg gly arg

145 GTG CAG GGT CTG CTG GAA GAG GAG GCG GCG GCG CGG
val gln gly leu leu glu glu glu ala ala ala arg

181 GGC CGC CTG GAG CGC ACC CGT CTC GGA GCG CTT GCG
gly arg leu glu arg thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
glu glu glu glu asp **asp glu asp asp asp asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp **ser** leu cys gly pro his **pro** gly gln

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Fig. 11 (continued)

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
 glu glu gly arg gly pro ala ala gly ser gly thr
 541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
 arg gln val phe ser met ala ala leu ser lys glu
 577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
 gly gly ser ala ser ser thr thr gly pro asp ser
 613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
 pro ser pro val pro leu pro pro gly lys pro ala
 649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
 leu pro gly ala asp gly thr pro phe gly cys pro
 685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
 ala gly arg lys glu lys pro ala asp pro val glu
 721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
 trp thr val met asp val val glu tyr phe thr glu
 757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
 ala gly phe pro glu gln ala thr ala phe gln glu
 793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
 gln glu ile asp gly lys ser leu leu leu met gln
 829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
 arg thr asp val leu thr gly leu ser ile arg leu
 865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
 gly pro ala leu lys ile tyr glu his his ile lys
 901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
 val leu gln gln gly his phe glu asp asp asp pro
 937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
 glu gly phe leu gly
 973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
 1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
 1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
 1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
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ATHEROSCLEROSIS

Fig. 11 (continued)

1117	TGC	TAC	CCC	CCC	ACC	CCG	TGT	GTG	TCT	CTG	CAC	CTG
1153	CCC	CCA	GCA	CAC	CCC	TCC	CGG	AGC	CTG	GAT	GTC	GCC
1189	TGG	GAC	TCT	GGC	CTG	CTC	ATT	TTG	CCC	CCA	GAT	CAG
1225	CCC	CCT	CCC	TCC	CTC	CTG	TCC	CAG	GAC	ATT	TTT	TAA
1261	AAG	AAA	AAA	AGG	AAA	AAA	AAA	AAT	TGG	GGA	GGG	GGC
1297	TGG	GAA	GGT	GCC	CCA	AGA	TCC	TCC	TCG	GCC	CAA	CCA
1333	GGT	GTT	TAT	TCC	TAT	ATA	TAT	ATA	TAT	ATG	TTT	TGT
1369	TCT	GCC	TGT	TTT	TCG	TTT	TTT	GGT	GCG	TGG	CCT	TTC
1405	TTC	CCT	CCC	ACC	ACC	ACT	CAT	GGC	CCC	AGC	CCT	GCT
1441	CGC	CCT	GTC	GGC	GGG	AGC	AGC	TGG	GAA	TGG	GAG	GAG
1477	GGT	GGG	ACC	TTG	GGT	CTG	TCT	CCC	ACC	CTC	TCT	CCC
1513	GTT	GGT	TCT	GTT	GTC	GCT	CCA	GCT	GGC	TGT	ATT	GCT
1549	TTT	TAA	TAT	TGC	ACC	GAA	GGG	TTG	TTT	TTT	TTT	TTT
1585	TAA	ATA	AAA	TTT	TAA	AAA	AAG	GAA	AAA	AAA	AAA	AAA

FOI b2 b7E 2001

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 12

256 GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
 ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
 gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
 glu glu glu glu asp **asp glu asp asp** asp asp **asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
 val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
 arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
 gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
 lys glu trp **ser leu** cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
 glu glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
 arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
 gly gly **ser** ala ser **ser thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
 pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
 leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
 ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
 trp thr val met asp val val glu tyr phe thr glu

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Fig. 12 (continued)

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG

1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC

1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG

1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA

1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC

1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA

1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT

1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC

1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT

1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG

1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC

1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT

1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT

1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 13

196 ACC CGT CTC GGA GCG CTT GCG
thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
glu glu glu glu asp **asp glu asp asp** asp asp **asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp **ser** leu cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
gly gly **ser** ala ser **ser thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
leu pro gly ala asp gly thr pro phe gly cys pro

10023529.121701

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 13 (continued)

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro ala asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG

1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC

1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG

1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA

1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC

1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA

1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT

1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC

1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT

1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG

1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC

1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT

1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT

1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

10023529.12701

LEVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 14

1	GTG	GAA	AAT	AGC	AAC	TGT	GTT	TCT	CAA	GGA	TCC	AAT
37	CCC	AAC	CTA	AGG	TGG	CAG	CGC	ACA	ATG	AAG	AAT	CAA
									met	lys	asn	gln
73	GAC	AAA	AAG	AAC	GGG	GCT	GCC	AAA	CAG	CCC	AAC	CCC
	asp	lys	lys	asn	gly	ala	ala	lys	gln	pro	asn	pro
109	AAA	AGC	AGC	CCG	GGA	CAG	CCG	GAA	GCA	GGA	GCG	GAG
	lys	ser	ser	pro	gly	gln	pro	glu	ala	gly	ala	glu
145	GGA	GCC	CAG	GGG	CGG	CCC	GGC	CGG	CCG	GCC	CCC	GCC
	gly	ala	gln	gly	arg	pro	gly	arg	pro	ala	pro	ala
181	CGA	GAA	GCC	GAA	GGT	GCC	AGC	AGC	CAG	GCT	CCC	GGG
	arg	glu	ala	glu	gly	ala	ser	ser	gln	ala	pro	gly
217	AGG	CCG	GAG	GGG	GCT	CAA	GCC	AAA	ACT	GCT	CAG	CCT
	arg	pro	glu	gly	ala	gln	ala	lys	thr	ala	gln	pro
253	GGG	GCG	CTC	TGT	GAT	GTC	TCT	GAG	GAG	CTG	AGC	CGC
	gly	ala	leu	cys	asp	val	ser	glu	glu	leu	ser	arg
289	CAG	TTG	GAA	GAC	ATA	CTC	AGT	ACA	TAC	TGT	GTG	GAC
	gln	leu	glu	asp	ile	leu	ser	thr	tyr	cys	val	asp
325	AAC	AAC	CAG	GGG	GCC	CCG	GGT	GAG	GAT	GGG	GTC	CAG
	asn	asn	gln	gly	ala	pro	gly	glu	asp	gly	val	gln
361	GGT	GAG	CCC	CCT	GAA	CCT	GAA	GAT	GCA	GAG	AAG	TCT
	gly	glu	pro	pro	glu	pro	glu	asp	ala	glu	lys	ser
397	CGC	GCC	TAT	GTG	GCA	AGG	AAT	GGG	GAG	CCG	GAG	CCG
	arg	ala	tyr	val	ala	arg	asn	gly	glu	pro	glu	pro
433	GGC	ACC	CCA	GTA	GTC	AAT	GGC	GAG	AAG	GAG	ACC	TCC
	gly	thr	pro	val	val	asn	gly	glu	lys	glu	thr	ser
469	AAG	GCA	GAG	CCG	GGC	ACG	GAA	GAG	ATC	CGG	ACG	AGC
	lys	ala	glu	pro	gly	thr	glu	glu	ile	arg	thr	ser
505	GAT	GAG	GTC	GGA	GAC	CGA	GAC	CAC	CGG	AGG	CCA	CAG
	asp	glu	val	gly	asp	arg	asp	his	arg	arg	pro	gln

Fig. 14 (continued)

541 GAA AAG AAG AAG GCC AAG GGT CTG GGA AAG GAG ATC
glu lys lys lys ala lys gly leu gly lys glu ile

577 ACG CTG CTG ATG CAG ACA CTG AAC ACG CTG AGC ACC
thr leu leu met gln thr leu asn thr leu ser thr

613 CCA GAG GAG AAG CTG GCG GCT CTG TGC AAG AAG TAT
pro glu glu lys leu ala ala leu cys lys lys tyr

649 GCG GAA CTG CTC GAG GAG CAC CGG AAC TCG CAG AAG
ala glu leu leu glu glu his arg asn ser gln lys

685 CAG ATG AAG CTG CTG CAG AAG AAG CAG AGC CAG CTG
gln met lys leu leu gln lys lys gln ser gln leu

721 GTG CAG GAG AAG GAC CAC CTG CGT GGC GAG CAC AGC
val gln glu lys asp his leu arg gly glu his ser

757 AAG GCC ATC CTG GCC CGC AGC AAG CTC GAG AGC CTG
lys ala ile leu ala arg ser lys leu glu ser leu

793 TGC CGG GAG CTG CAG CGG CAC AAC CGC TCG CTC AAG
cys arg glu leu gln arg his asn arg ser leu lys

829 GAA GAA GGT GTG CAG CGA GCC CGA GAG GAG GAG GAG
glu glu gly val gln arg ala arg glu glu glu glu

865 AAG CGC AAG GAG GTG ACG TCA CAC TTC CAG ATG ACG
lys arg lys glu val thr ser his phe gln met thr

901 CTC AAC GAC ATT CAG CTG CAG ATG GAG CAG CAC AAC
leu asn asp ile gln leu gln met glu gln his asn

937 GAG CGC AAC TCC AAG CTG CGC CAG GAG AAC ATG GAG
glu arg asn ser lys leu arg gln glu asn met glu

973 CTG GCC GAG CGG CTC AAG AAG CTG ATT GAG CAG TAC
leu ala glu arg leu lys lys leu ile glu gln tyr

1009 GAG CTG CGA GAA GAG CAC ATC GAC AAA GTC TTC AAA
glu leu arg glu glu his ile asp lys val phe lys

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Fig. 14 (continued)

1045 CAC AAG GAT CTG CAG CAG CAG CTG GTG GAC GCC AAG
his lys asp leu gln gln gln leu val asp ala lys

1081 CTC CAG CAG GCC CAG GAG ATG CTG AAG GAG GCA GAG
leu gln gln ala gln glu met leu lys glu ala glu

1117 GAG CGG CAC CAG CGG GAG AAG GAC TTT CTC CTG AAG
glu arg his gln arg glu lys asp phe leu leu lys

1153 GAG GCC GTG GAG TCC CAG AGG ATG TGC GAG CTG ATG
glu ala val glu ser gln arg met cys glu leu met

1189 AAG CAA CAG GAG ACC CAC CTG AAG CAG CAG CTT GCC
lys gln gln glu thr his leu lys gln gln leu ala

1225 CTA TAC ACA GAG AAG TTT GAG GAG TTC CAG AAC ACT
leu tyr thr glu lys phe glu glu phe gln asn thr

1261 CTT TCC AAA AGC AGC GAG GTG TTC ACC ACA TTC AAA
leu ser lys ser ser glu val phe thr thr phe lys

1297 CAG GAA ATG GAA AAG ATG ACA AAG AAG ATC AAG AAG
gln glu met glu lys met thr lys lys ile lys lys

1333 CTG GAG AAA GAG ACC ACC ATG TAC CGT TCC CGG TGG
leu glu lys glu thr thr met tyr arg ser arg trp

1369 GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG
glu ser ser asn lys ala leu leu glu met ala glu

1405 GAG AAA ACA CTC CGG GAC AAA GAG CTG GAA GGC CTG
glu lys thr leu arg asp lys glu leu glu gly leu

1441 CAG GTG AAA ATC CAG CGG CTG GAG AAG CTG TGC CGG
gln val lys ile gln arg leu glu lys leu cys arg

1477 GCA CTG CAG ACA GAG CGC AAT GAC CTG AAC AAG AGG
ala leu gln thr glu arg asn asp leu asn lys arg

1513 GTG CAG GAC CTG AGT GCC GGT GGC CAG GGC CCC GTC
val gln asp leu ser ala gly gly gln gly pro val

1002329-12701

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 14 (continued)

1549 TCC GAC AGC GGT CCT GAG CGG AGG CCA GAG CCC GCC
 ser asp ser gly pro glu arg arg pro **glu pro ala**
 1585 ACC ACC TCC AAG GAG CAG GGT GTC GAG GGC CCC GGG
 thr thr ser lys glu gln gly val glu gly pro gly
 1621 GCT CAA GTA CCC AAC TCT CCA AGG GCC ACA GAC GCT
 ala gln **val** pro **asn** ser pro arg **ala** thr **asp** ala
 1657 TCC TGC TGC GCA GGT GCA CCC AGC ACA GAG GCA TCA
 ser cys **cys ala** gly ala pro ser thr glu ala ser
 1693 GGC CAG ACA GGG CCC CAG GAG CCC ACC ACT GCC ACT
 gly gln thr gly pro gln glu pro thr **thr** ala **thr**
 1729 GCC TAG AGA GCT TGG TGC TGG GGT GTG CCA GGA AGG
 ala
 1765 GAG CAG GCA GCC CAG CCA GGC CTG GCC CAG CCC AGG
 1801 CTC CCA TGC TAA GCA GTC CGG TGC TGA GGC CAG GAT
 1837 GTT CTG ACC TGG CTG GCA CCT GAC CCT CTG CAG TCT
 1873 TGG ATT TTG TGG GTC AGT TTT ACA TGC ATA TGG CAC
 1909 ACA TGC AAG GCC TCA CAC ATT TGT GTC TCT AAG TGT
 1945 ACT GTG GGC TTG CAT CGG GGG TGA CGA TGG ACA GAT
 1981 GAA GCC AGC GGC TCC CTT GTG AGC TGA AGT CTT ACG
 2017 GAG GAG ACG GCG TCT GCA CTG CCA TCG CAG TGA CCT
 2053 GCA GGA CGA GTT CCT TGA GCT TTC CCT GCC TGC TTT
 2089 GAG GCT GAG ACC CCT CCC GGC CCT TCA GAG CTC CTG
 2125 ACA GGT GAT ACA CAC CCA GCC TTG ACC GCA CTT CTC
 2161 TTG GGT AGC TGG GCT CTC CTA GCC TCC CCC AGA GGC
 2197 GCC ATT GCT TCT CTT GAC TTG GAG AGG GGA TGC CCA
 2233 GGC GTG GCC TTG GCA GGC ACT GGG AGC TAG TGA TTG
 2269 GGC TGC TCT CCT GCC TCG AGC AGG GGC AGG AGT GTT
 2305 TCT GGT GGG ATG ATG CGC TCG CTG GTC AGG AGC CCC
 2341 GTG GGC GCT GCT TCC CCC GCC CTC TGG TGA TGC CAG
 2377 GAC CAG GCC AGT GAT GCT TCT CAG TAG CCT TAC CAT
 2413 TCA CAG GTG CCT CTC CAG CCC GCA CAG TGA GTG ACA
 2449 AGA TCA TCC AAA GGA TTC CTT CTG AAG GTG TTC GTT
 2485 TCG TTT TGT TTT GTT GCA CGT GAC GGT TTG TAT TGA
 2521 GGA CCC TCT GAG GAA GAG GGG TGC TGT AGC AGT GGT
 2557 CCC TGC GTG CCT GGC TCC AGT GTC CTG CCC TCC CCC
 2593 CCC TCG CCA TGG CTC CTC GGC CGC CTT GGT GCT GAG
 2629 GTT TCT GTT TGG TGA GAT CAG GTT GTC TGT TCA GAG

10023529.12101

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 14 (continued)

2665 AGA AGA GGC GTC TGA TGG CTT TGC CGC CAG CTT GCC
2701 TGC GGG CCT CAA TCC CGG GAG GCC GCC CGG TTC CCG
2737 TCA CTG TTG TCC CCG TGC AGT GCG TTG CTG GTC CCC
2773 AGG ACC AGC TGC TCG TTT GCT GTA TGG GTC AGT TTC
2809 TGC TTC CTG CCC CCC ACT CCA CCT AAC TGC AAT CCT
2845 TGG GGT TTC CCT GGT TCT CGT CCC TGG TAC CTC TGT
2881 GCC CAA GAA GTA GCC TTC TTT GGG ATT CTT GTT CTG
2917 CCC ATG CGG GAG CTG CTG CTG TCT GAC AGG TGA GGC
2953 CTG AGA CTC AGC GGC TGA CAG AGC TGC AGA GCT CTG
2989 CAC GGT GGC TCC CGG GGC GGC CTC TGT GTG CTG CAC
3025 ACC GCT GCT CTG CTG GCA CTG GCC AGT CTG TGC AGA
3061 GCA TTT GAG TAC TGG CTC AGG AGG GAG GGC TCT GCT
3097 GGC CTC GAG GGA CAG CGC CAC GTC TCC AGC TGG GCT
3133 CAG GGA GAG CCC CAG ACT GGC TGC GTA GGG TGC TTG
3169 GGG TTT GCT TCT TGC AGT ATT TCT TGG AAG CTG TTT
3205 TGT TGT CCT GCT ATT CCT TCA TCT TCC ACA GTC CAC
3241 GCT CAG CCT TTA ACT TGG ATC CCT CAC ATA ACA GGG
3277 TTC ATG AGA CCC GCA AGT ACG CCC AAG CTA CGT ATG
3313 GCT GAG GCC AGC TGG CAG GTG AAT GGC ACG CCA TTG
3349 CTG CTG CTA ATC CCT GGC ATA TCT TTA GTT CAC CTC
3385 GAA ATG CCC CCG CCA CAG TGC AAG CAG TGA GTC CAC
3421 GTG CCA CCC TGG GCT GAA TCC CAC CCC CTG TGA GTG
3457 TTG CCC GAG ATT GTG TCT CTT CTG AAT GCC TTC ACT
3493 GGG AAT GGC CTC TGC CGC CTC CTG CTC AGG GAG GCT
3529 TTC CCC TTC CCT CAG CCC CTG TGC CAG ACT GAG GTA
3565 CAA GAA CCG CCA AGC CCA TGC AAG GTG TGG CTA GGC
3601 GCC AGG GTG CAG GAA GGA GGC AGG TAG CTG CCT GCA
3637 CCC TTG AAA GCC AAG AGG CCT ACG GTG GCC TCC ATC
3673 CTG GCT TGC CTC ACT TCA GCT ACC TCG CAT AGC CCA
3709 GGG GTG GGG CTA TTG GAT TCC AGG GTG GGG GGA TGG
3745 GAA GCT GCA GGG GGC AGG TGG CTC TCA CTA GGC TTC
3781 CCA GCT CAG GAA TGT GGG CCT CAG GTA GGG GAG AGC
3817 CTT TGC TCC ACT CCA CCC ATT TGC AGG CAT CTA GGC
3853 CAG TCT AGA TGG CGA CCC CTT CTC TTC CTC TCC ATT
3889 GAC CAA ATC GTA CCT GTC TCT CCA GCT GCT CGC TTG
3925 CTC TGC TTT CCA AAG TCA GCC CAG GTA CCC AGG TGC
3961 CGC CCA CAT TGG CCT GGA ACC TGG ACC AGA GGC AAG
3997 GGA GGT GGC CTA TCC TTG AGT GAT AGC CAG TGC CTT
4033 CCT CAC CCG GTG GCT TCC ATG CCT GTG ACC TCA GAT
4069 TTA GGA CCA AGA GCT GTG TTG GTT TCT TAC GTT GTG
4105 AGC TTT CCC TCC AGG GGA CCA CAG CAG GTG AGG CTC
4141 GGA GCC CAG AGC CCT TGG CGC CGC CAG CAG TAA CTT
4177 GTG TCC GGA CCT TGT CCA GCT GAG CGC TTC GTG TAT

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 14 (continued)

4213	GAC	TCA	GCT	TCG	TGT	GTG	AGT	CCA	GCG	GAG	TGC	GTC
4249	ACG	TGA	CCT	AGA	CTC	AGC	GGT	GTC	AGC	CGC	ACT	TTG
4285	ATT	TGT	TTG	TTT	TCC	ATG	AGG	TTT	TTG	GAC	CAT	GGG
4321	CTT	AGC	TCA	GGC	AAC	TTT	TCT	GTA	AGG	AGA	ATG	TTA
4357	ACT	TTC	TGT	AAA	GAT	GCT	TAT	TTA	ACT	AAC	GCC	TGC
4393	TTC	CCC	CAC	TCC	CAA	CCA	GGT	GGC	CAC	CGA	GAG	CTC
4429	ACC	AGG	AGG	CCA	ATA	GAG	CTG	CTC	CAG	CTC	TCC	CAT
4465	CTT	GCA	CCG	CAC	AAA	GGT	GGC	CGC	CCC	AGG	GAC	AGC
4501	CAG	GCA	CCT	GCC	TGG	GGG	AGG	GGC	TTC	TCT	TCC	TTA
4537	TGG	CCT	GGC	CAT	CTA	GAT	TGT	TTA	AAG	TTG	TGC	TGA
4573	CAG	CTT	TTT	TTG	GTT	TTT	TGG	TTT	TTG	TTT	TTG	TTT
4609	TTG	TTT	TTG	TTT	TTG	TCT	ACT	TTT	GGT	ATT	CAC	AAC
4645	AGC	CAG	GGA	CTT	GAT	TTT	GAT	GTA	TTT	TAA	GCC	ACA
4681	TTA	AAT	AAA	GAG	TCT	GTT	GCC	TTA	AAA	AAA	AAA	AAA
4717	AAA	AAA										

1003529-101701

Fig. 15

1 GAC GCC TCA GAG CGG AAC AGG GAA GTG AAT CAG GCG
37 CCG GGT AGT GGG TTG CTG GGC TGG GCT TGC TGA GGT
73 AGA GGC AGC GCC AAG AAG AGG CCT TTG CCG CTG GTC
109 GGG ATT GGG ATG TCG AAG AAC ACA GTG TCG TCG GCC
met ser lys asn thr val ser ser ala

145 CGC TTC CGG AAG GTG GAC GTG GAT GAA TAT GAC GAG
arg phe arg lys val asp val asp glu tyr asp glu

181 AAC AAG TTC GTG GAC GAA GAA GAT GGG GGC GAC GGC
asn lys phe val asp glu glu asp gly gly asp gly

217 CAG GCC GGG CCC GAC GAG GGC GAG GTG GAC TCC TGC
gln ala gly pro asp glu gly glu val asp ser cys

253 CTG CGG CAA GGA AAC ATG ACA GCT GCC CTA CAG GCA
leu arg gln gly asn met thr ala ala leu gln ala

289 GCT CTG AAG AAC CCC CCT ATC AAC ACC AAG AGT CAG
ala leu lys asn pro pro ile asn thr lys ser gln

325 GCA GTG AAG GAC CGG GCA GGC AGC ATT GTC TTG AAG
ala val lys asp arg ala gly ser ile val leu lys

361 GTG CTC ATC TCT TTT AAA GCT AAT GAT ATA GAA AAG
val leu ile ser phe lys ala **asn** asp ile glu lys

397 GCA GTT CAA TCT CTG GAC AAG AAT GGT GTG GAT CTC
ala val gln ser leu asp **lys** asn gly val asp leu

433 CTA ATG AAG TAT ATT TAT AAA GGA TTT GAG AGC CCG
leu met lys tyr ile tyr lys gly phe glu ser pro

469 TCT GAC AAT AGC AGT GCT ATG TTA CTG CAA TGG CAT
ser asp **asn** ser ser ala **met** leu leu gln trp his

505 GAA AAG GCA CTT GCT GCT GGA GGA GTA GGG TCC ATT
glu lys ala leu ala ala gly gly val gly ser ile

541 GTT CGT GTC TTG ACT GCA AGA AAA ACT GTG TAG TCT
val arg val leu thr ala arg lys thr val

1003369:13701

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 15 (continued)

577 GGC AGG AAG TGG ATT ATC TGC CTC GGG AGT GGG AAT
613 TGC TGG TAC AAA GAC CAA AAC AAC CAA ATG CCA CCG
649 CTG CCC TGT GGG TAG CAT CTG TTT CTC TCA GCT TTG
685 CCT TCT TGC TTT TTC ATA TCT GTA AAG AAA AAA ATT
721 ACA TAT CAG TTG TCC CTT TAA TGA AAA TTG GGA TAA
757 TAT AGA AGA AAT TGT GTT AAA ATA GAA GTG TTT CAT
793 CCT TTC AAA ACC ATT TCA GTG ATG TTT ATA CCA ATC
829 TGT ATA TAG TAT AAT TTA CAT TCA AGT TTT AAT TGT
865 GCA ACT TTT AAC CCT GTT GGC TGG TTT TTG GTT CTG
901 TTT GGT TTT GTA TTA TTT TTA ACT AAT ACT GAA AAA
937 TTT GGT CAG AAT TTG AGG CCA GTT TCC TAG CTC ATT
973 GCT AGT CAG GAA ATG ATA TTT ATA AAA AAT ATG AGA
1009 GAC TGG CAG CTA TTA ACA TTG CAA AAC TGG ACC ATA
1045 TTT CCC TTA TTT AAT AAG CAA AAT ATG TTT TTG GAA
1081 TAA GTG GTG GGT GAA TAC CAC TGC TAA GTT ATA GCT
1117 TTG TTT TTG CTT GCC TCC TCA TTA TCT GTA CTG TGG
1153 GTT TAA GTA TGC TAC TTT CTC TCA GCA TCC AAT AAT
1189 CAT GGC CCC TCA ATT TAT TTG TGG TCA CGC AGG GTT
1225 CAG AGC AAG AAG TCT TGC TTT ATA CAA ATG TAT CCA
1261 TAA AAT ATC AGA GCT TGT TGG GCA TGA ACA TCA AAC
1297 TTT TGT TCC ACT AAT ATG GCT CTG TTT GGA AAA AAC
1333 TGC AAA TCA GAA AGA ATG ATT TGC AGA AAG AAA GAA
1369 AAA CTA TGG TGT AAT TTA AAC TCT GGG CAG CCT CTG
1405 AAT GAA ATG CTA CTT TCT TTA GAA ATA TAA TAG CTG
1441 CCT TAG ACA TTA TGA GGT ATA CAA CTA GTA TTT AAG
1477 ATA CCA TTT AAT ATG CCC CGT AAA TGT CTT CAG TGT
1513 TCT TCA GGG TAG TTG GGA TCT CAA AAG ATT TGG TTC
1549 AGA TCC AAA CAA ATA CAC ATT CTG TGT TTT AGC TCA
1585 GTG TTT TCT AAA AAA AGA AAC TGC CAC ACA GCA AAA
1621 AAT TGT TTA CTT TGT TGG ACA AAC CAA ATC AGT TCT
1657 CAA AAA ATG ACC GGT GCT TAT AAA AAG TTA TAA ATA
1693 TCG AGT AGC TCT AAA ACA AAC CAC CTG ACC AAG AGG
1729 GAA GTG AGC TTG TGC TTA GTA TTT ACA TTG GAT GCC
1765 AGT TTT GTA ATC ACT GAC TTA TGT GCA AAC TGG TGC
1801 AGA AAT TCT ATA AAC TCT TTG CTG TTT TTG ATA CCT
1837 GCT TTT TGT TTC ATT TTG TTT TGT TTT GTA AAA ATG
1873 ATA AAA CTT CAG AAA ATA AAA TGT CAG TGT TGA ATA
1909 ATT AAA AAA AAA AAA AA

1003539.2401

Fig. 16

1 GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT
glu glu arg val leu glu lys glu glu glu glu **asp**

37 GAT GAT GAA GAT GAA GAT GAA GAA GAT GAT GTG TCA
asp asp glu asp **glu asp glu glu** asp asp val ser

73 GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA
glu gly ser glu val pro glu ser asp arg pro ala

109 GGT GCC CAG CAC CAC CAG CTT AAC GGC GAG CGG GGA
gly ala gln his his gln leu asn gly glu arg gly

145 CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**

181 CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG
pro cys gly pro his **gln** gly gln **asp** glu gly arg

217 GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC
gly pro ala **pro** gly ser gly thr arg gln val phe

253 TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT
ser met ala ala **met asn** lys glu gly gly **thr** ala

289 TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG
ser **val ala** thr gly pro asp ser pro ser pro val

325 CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC
pro leu pro pro gly lys pro ala leu pro gly ala

361 GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA
asp gly thr pro phe gly cys pro **pro** gly arg lys

397 GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG
glu lys pro **ser** asp pro val glu trp thr val met

433 GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG
asp val val glu tyr phe thr glu ala gly phe pro

469 GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT
glu gln ala thr ala phe gln glu gln glu ile asp

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 16 (continued)

505	GGC gly	AAA lys	TCT ser	TTG leu	CTG leu	CTC leu	ATG met	CAG gln	CGC arg	ACA thr	GAT asp	GTG val
541	CTC leu	ACC thr	GGC gly	CTG leu	TCC ser	ATC ile	CGC arg	CTC leu	GGG gly	CCA pro	GCC ala	CTG leu
577	AAA lys	ATC ile	TAC tyr	GAG glu	CAC his	CAC his	ATC ile	AAG lys	GTG val	CTT leu	CAG gln	CAA gln
613	GGC gly	CAC his	TTT phe	GAG glu	GAT asp	GAT asp	GAC asp	CCC pro	GAT asp	GGC gly	TTC phe	TTA leu
649	GGC gly	TGA	GCG	CCC	AGC	CTC	ACC	CCT	GCC	CCA	GCC	CAT
685	TCC	GGC	CCC	CAT	CTC	ACC	CAA	GAT	CCC	CCA	GAG	TCC
721	AGG	AGC	TGG	ACG	GGG	ACA	CCC	TCA	GCC	CTC	ATA	ACA
757	GAT	TCC	AAG	GAG	AGG	GCA	CCC	TCT	TGT	CCT	TAT	CTT
793	TGC	CCC	TTG	TNT	CTG	TCT	CAC	ACA	CAT	CTG	CTC	CTC
829	AGC	ACG	TCG	GTG	TGG	GGA	GGG	GAT	TGC	TCC	TTA	AAC
865	CCC	AGG	TGG	CTG	ACC	CTC	CCC	ACC	CAG	TCC	AGG	ACA
901	TTT	TAG	GAA	AAA	AAA	AAT	GAA	ATG	TGG	GGG	GCT	TCT
937	CAT	CTC	CCC	AAG	ATC	CTC	TTC	CGT	TCA	GCC	AGA	TGT
973	TTC	CTG	TAT	AAA	TGT	TTG	GAT	CTG	CCT	GTT	TAT	TTT
1009	GGT	GGG	TGG	TCT	TTC	CTC	CCT	CCC	CTA	CCA	CCC	ATG
1045	CCC	CCC	TTC	TCA	GTC	TGC	CCC	TGG	CCT	CCA	GCC	CCT
1081	AGG	GGA	CTA	GCT	GGG	TTG	GGG	TTC	CTC	GGG	CCT	TTT
1117	CTC	TCC	TCC	CTC	TTT	TCT	TTC	TGT	TGA	TTG	TCG	CTC
1153	CAG	CTG	GCT	GTA	TTG	CTT	TTT	AAT	ATT	GCA	CCG	AAG
1189	GTT	TTT	TAA	ATA	AAA	TTT	TA					

Fig. 17

1 CA AAA AGC AGC CCA GGA CAA CCG GAA GCA GGA CCC GAG GGA GCC
lys ser ser pro gly gln pro glu ala gly **pro** glu gly ala

45 CAG GAG CGG CCC AGC CAG GCG GCT CCT GCA GTA GAA GCA GAA GGT
gln **glu** arg pro **ser** **gln** **ala** ala pro ala **val** glu ala glu gly

90 CCC GGC AGC AGC CAG GCT CCT CGG AAG CCG GAG GGG GCT CAA GCC
pro **gly** ser ser gln ala pro **arg** **lys** pro glu gly ala gln ala

135 AGA ACG GCT CAG TCT GGG GCC CTT CGT GAT GTC TCT GAG GAG CTG
arg thr ala gln **ser** gly ala leu **arg** asp val ser glu glu leu

180 AGC CGC CAA CTG GAA GAC ATA CTG AGC ACA TAC TGT GTG GAC AAT
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn

225 AAC CAG GGG GGC CCC GGC GAG GAT GGG GCA CAG GGT GAG CCG GCT
asn gln gly **gly** pro gly glu asp gly **ala** gln gly glu pro **ala**

270 GAA CCC GAA GAT GCA GAG AAG TCC CGG ACC TAT GTG GCA AGG AAT
glu pro glu asp ala glu lys ser arg **thr** tyr val ala arg asn

315 GGG GAG CCT GAA CCA ACT CCA GTA GTC TAT GGA GAG AAG GAA CCC
gly glu pro glu pro thr pro val val **tyr** gly glu lys glu **pro**

360 TCC AAG GGG GAT CCA AAC ACA GAA GAG ATC CGG CAG AGT GAC GAG
ser lys **gly** **asp** pro **asn** thr glu glu ile arg **gln** ser asp glu

405 GTC GGA GAC CGA GAC CAT CGA AGG CCA CAG GAG AAG AAA AAA GCC
val gly asp arg asp his arg arg pro gln glu lys lys lys ala

450 AAG GGT TTG GGG AAG GAG ATC ACG TTG CTG ATG CAG ACA TTG AAT
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn

495 ACT CTG AGT ACC CCA GAG GAG AAG CTG GCT GCT CTG TGC AAG AAG
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys

540 TAT GCT GAA CTG CTG GAG GAG CAC CGG AAT TCA CAG AAG CAG ATG
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met

585 AAG CTC CTA CAG AAA AAG CAG AGC CAG CTG GTG CAA GAG AAG GAC
lys leu leu gln lys lys gln ser gln leu val gln glu lys asp

630 CAC CTG CGC GGT GAG CAC AGC AAG GCC GTC CTG GCC CGC AGC AAG
his leu arg gly glu his ser lys ala **val** leu ala arg ser lys

675 CTT GAG AGC CTA TGC CGT GAG CTG CAG CGG CAC AAC CGC TCC CTC
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 17 (continued)

720 AAG GAA GAA GGT GTG CAG CGG GCC CGG GAG GAG GAG GAG AAG CGC
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg

765 AAG GAG GTG ACC TCG CAC TTC CAG GTG ACA CTG AAT GAC ATT CAG
lys glu val thr ser his phe gln val thr leu asn asp ile gln

810 CTG CAG ATG GAA CAG CAC AAT GAG CGC AAC TCC AAG CTG CGC CAA
leu gln met glu gln his asn glu arg asn ser lys leu arg gln

855 GAG AAC ATG GAG CTG GCT GAG AGG CTC AAG AAG CTG ATT GAG CAG
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln

900 TAT GAG CTG CGC GAG GAG CAT ATC GAC AAA GTC TTC AAA CAC AAG
tyr glu leu arg glu glu his ile asp lys val phe lys his lys

945 GAC CTA CAA CAG CAG CTG GTG GAT GCC AAG CTC CAG CAG GCC CAG
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln

990 GAG ATG CTA AAG GAG GCA GAA GAG CGG CAC CAG CGG GAG AAG GAT
glu met leu lys glu ala glu glu arg his gln arg glu lys asp

1035 TTT CTC CTG AAA GAG GCA GTA GAG TCC CAG AGG ATG TGT GAG CTG
phe leu leu lys glu ala val glu ser gln arg met cys glu leu

1080 ATG AAG CAG CAA GAG ACC CAC CTG AAG CAA CAG CTT GCC CTA TAC
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr

1125 ACA GAG AAG TTT GAG GAG TTC CAG AAC ACA CTT TCC AAA AGC AGC
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

1170 GAG GTA TTC ACC ACA TTC AAG CAG GAG ATG GAA AAG ATG ACT AAG
glu val phe thr thr phe lys gln glu met glu lys met thr lys

1215 AAG ATC AAG AAG CTG GAG AAA GAA ACC ACC ATG TAC CGG TCC CGG
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg

1260 TGG GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG GAG AAA
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys

1305 ACA GTC CGG GAT AAA GAA CTG GAG GGC CTG CAG GTA AAA ATC CAA
thr val arg asp lys glu leu glu gly leu gln val lys ile gln

1350 CGG CTG GAG AAG CTG TGC CGG GCA CTG CAG ACA GAG CGC AAT GAC
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp

1395 CTG AAC AAG AGG GTA CAG GAC CTG AGT GCT GGT GGC CAG GGC TCC
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser

1440 CTC ACT GAC AGT GGC CCT GAG AGG AGG CCA GAG GGG CCT GGG GCT
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 17 (continued)

1485 CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA
gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro

1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu

1575 CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG
pro thr ser ala arg ala ***

1620 GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC
1665 CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG
1710 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA
1755 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT
1800 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA
1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC
1890 TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG
1935 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT
1980 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG
2025 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG
2070 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA
2115 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG
2160 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT
2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA
2250 GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT
2295 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG
2340 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT TTT
2385 TTT TTT CTT TTT CTT TTT TTT TTG CAC ATG ACA GTG TTT GTA TTG
2430 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT
2475 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC
2520 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT
2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC
2610 AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC
2655 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG
2700 CTG CTT CTT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC
2745 CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC
2790 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG
2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG
2880 ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT
2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG
2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG
3015 CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA
3060 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT
3105 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT
3150 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT
3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT
3240 GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC
3285 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC
3330 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA
3375 GCT GTG TGA TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG
3420 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TTC CCC TTT GAA
3465 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTC TTG CTC CAG TAG

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 17 (continued)

3510 GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA
3555 GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG
3600 AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG
3645 CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT
3690 CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT
3735 GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC
3780 AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA
3825 GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT
3870 CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA
3915 CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC
3960 AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC
4005 CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC
4050 AAG ATC TGT GTT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG
4095 ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA
4140 AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA
4185 GAT TCT GAG AGG TGT CAG CAG CAC TTT TTT TTT TTA TTT GTT GTT
4230 TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT
4275 TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC
4320 CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT
4365 GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT
4410 GAT TCT CCA GCT GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG
4455 AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT
4500 TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT
4545 TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC
4590 AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA
4635 TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT
4680 AAA AAA AAA AAA AAA AAA

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Fig. 18

GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG
val asp val asp glu tyr asp glu asn lys phe val

GAC GAG GAA GAC GGC GGC GAC GGC
asp glu glu asp gly gly asp gly

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 19

	1		50
Rabbit	MSKNTVSSAR FRKVDVDEYD ENKFVDEEDG GDGQAGPDEG	EVDSCLRQGN	
Human	
	51		100
Rabbit	MTAALQAALK NPPINTRSQA VKDRAGSIVL KVLISFKAGD	IEKAVQSLDR	
HumanK...N.K	
	101		150
Rabbit	NGVDLLMKYI YKGFESPSDN SSAVLLQWHE KALAAGGVGS	IVRVLTARKT	
HumanM.....	
	151		
Rabbit	V		
Human	.		

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 20

	1		50
Rabbit	EERVLEKEEEE EEEEEDEDD DDDVVSEGSE VPESDRPAGA QHHQLNGGER		
HumanDDD..EDEE ..--.....		
	51		100
Rabbit	GPQTAKERAK EWSLCGPHPG QEEGRGPAAG SGTRQVFSMA ALSKEGGSAS		
Human	...S....V. ..TP....Q. .D.....P.MN....T..		
	101		150
Rabbit	STTGPDSPSP VPLPPGKPAL PGADGTPFGC PAGRKEKPAD PVEWTVMDVV		
Human	VA..... .P.....S.		
	151		200
Rabbit	EYFTEAGFPE QATAFQEQEI DGKSLLLMQR TDVLTGLSIR LGPALKIYEH		
Human		
	201	220	
Rabbit	HIKVLQQGHF EDDDPEGFLG		
HumanD....		

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fig. 21

	1	50
Rabbit	MKNQDKKNGA AKQPNPKSSP GQPEAGAEGA QGRPGRPAPA REAEG-ASSQ	
Human	-----P... .E..SQA... V....PG...	
	51	100
Rabbit	APGRPEGAQA KTAQPGALCD VSEELSRQLE DILSTYCVDN NQGAPGEDGV	
Human	..RK..... R...S...R.G.....A	
	101	150
Rabbit	QGEPPPEPEDA EKSRAYVARN GEPEPGTPVV NGEKETSKEAE PGTEEIRTSD	
HumanA..... .T..... Y....P..GD .N.....Q..	
	151	200
Rabbit	EVGDRDHRRP QEKKKAKGLG KEITLLMQTL NTLSTPEEKL AALCKKYAEL	
Human	
	201	250
Rabbit	LEEHRNSQKQ MKLLQKKQSQ LVQEKDHLRG EHSKAILARS KLESLCRELQ	
HumanV....	
	251	300
Rabbit	RHNRSLEKEG VQRAREEEEEK RKEVTSHFQM TLNDIQLQME QHNERNKSLR	
HumanV	
	301	350
Rabbit	QENMELAERL KKLIEQYELR EEHIDKVFKH KDLQQQLVDA KLQQAQEMLK	
Human	
	351	400
Rabbit	EAEERHQREK DFLLEAVES QRMCELMKQQ ETHLKQQLAL YTEKFEEFQN	
Human	
	401	450
Rabbit	TLKSSEVFT TFKQEMEKMT KKIKKLEKET TMYRSRWESS NKALLEMAEE	
Human	
	451	500
Rabbit	KTLRDKELEG LQVKIQRLK LCRALQTERN DLNKRVDLS AGGQGPVSDS	
Human	..V..... .SLT..	
	501	550
Rabbit	GPERRPEPAT TSKEQGVGEP GAQVPNSPRA TDASCCAGAP STEASGQTGP	
HumanA.S...V .E.P.YP....	
	551	
Rabbit	QEPTTATA	
HumanS.R.	

100333-1301

Applicant(s): Ann M. Lees et al.

HIGHER DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 22 (1/5)

1 AAGCTTTATAAAGATTTAACTACCTAATAAGGTAGAGAAGTAATTTATGTGCCCACTAAA 60
61 AAATACTCAATTTCTGAATGTTTCGTCCAAAATTAAGTGTGAGATCATTAAATCATTGAC 120
121 TAGAAACACGTTGAGTACCTATTATGTACTAGGCACCTAGATCATTGTGAGACATAAAA 180
181 AATACTGCATTAGAAAAGGACATTTTTCACATCTTAAATGCAATAAGCATTATTTGGCTG 240
241 GCAGTTAATTACATTTAACACATTAAACATATAGAGCAAAATTTCTGAGCAATCAAAATAA 300
301 TTATACCCCTTGAGCAATCGATTATTTAAATTTCTTTCACTATTCCCTTAAGCTGATTTCT 360
361 ACTCTGGGATTCTTTTCATAGTTCTCAAATAAGAAAAATAAAAAATTTCTAAATAAGGCAA 420
421 TACAAAAGAATAGAAAATGTAAGAGAAGAGATATATTAGCTCTTGAATCCCTGTTTCCATT 480
481 TGCTGTCAATAGTGCCTCTAATGTTTCGATTTTCTCTCAAAGAAAAATCTTGATTTAAAA 540
541 GGAAGAAAAAGTACAATCACCTTTAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT 600
601 TAGCAAAGACTGAAACTGAAAAAAATTTGTAATAATCTTTATTCTAAGTTATATAACGCCA 660
661 TTCACCATAGTAATGATTTTATACTTTGGTATATGGCTTTTTTAAATAAAATATTGCCAAC 720
721 AGGTAAAAATTTTCTTTGCTGTCTTAAGGCATTCCCTAAGAGAATTTTTTACCAGTGTGT 780
781 GTTCATAACTTGAATGTTAATTTAAACAATGTTACTTCTATCACCTAAATGATATACTTA 840
841 TAGAAGAGTGGTTTAATTTGGGAACAGAAAAACACCACATTGCTTCTTCCCAAGAAAAAGG 900
901 GATGTATTCCATTCTCGAGGTCTCTCTCCCACTCTCTATTTATATATAATATACTGCATA 960
961 GATAAATATACACACATTATATATGATTTTTTTTGAAGTAAAGAAGACTGGACATATGT 1020
1021 ATTTACATGTATATATCAACAAATTTAATTTTGAAGTCTCTCTCCCTCTCTGATTT 1080
1081 ATTATTCTCAGTATGAATTTCTCAAACGTACGGTCTTTTACATTTTCAATTCATTCAAG 1140
1141 CATGTATCGAGTCCCTTCTGCATGCTTAGCTTTTTTGTATATGGAAGGAAGATACAAAAAG 1200
1201 AAAAAGTGTCTTCTGCCCTTCAGAACTCTTTCCATCTCTTCTAGGAAGGAGATAAAACACCA 1260
1261 TATATCATTAAGAAATTTATAAGACTAGTCCCAAAACCAATGGTACAAGCAACATGCATT 1320
1321 TTACATTTATGTAGAATTTTAGAGCTTGGAACACTTTCGTGATATATAATCCTAAGAAC 1380
1381 AATCTTGTAAGTGCACATTATTAGCTCCATTTTCAGTGATGAGGAATCTGAGACAGAATT 1440
1441 TTAAGTGACATGTCTCGTTCAAACATTATGAGTGGAAGAGTCAACACTTAAGCCTGAGTT 1500
1501 TTCTGATTCTAAGCCTAGTGCTCTTTTCAACACAGCACTGGAAACCAAGATTGTGGTAC 1560
1561 ACAACAAGGCAACAGCCAGTCTTCTTGCTCGAGGTCCAACCTAAACTGGACCCATACCGAG 1620
1621 CAGTGTCCAGCCAAATGTCCAAATTAATTTTATCCTGCAAAATATTTGTTCTTCAGTGTA 1680
1681 TACACACAGCACAACTACCATTTTCTTCTGCTCTTAGTGCTTTATCTCTTACATTCCAGAA 1740
1741 ATGGGGATGTCAAATATTTTTTTAAATCTGGCCTAGATGGAATCATATAAATCTCAAATC 1800
1801 ATAATATAAATCTTAAAGGTCTGGTTTCCACCAATCCTTCCACATTTTGTCTTCCCCCAG 1860
1861 CACTAGAGAGCCTAACCTACCTTCCACCTTTCGAGCATTCTTGCTCCAAACGACCACT 1920
1921 ATTTTAAGATGTCAATGACCTTTCCCAATTTCTACAAATTCACCCAGTTTTGCCACCC 1980
1981 GACCCAGCGCCTGCCCGGACACGTTCCCTCCCTCCCAATAGATTTGATACCGAGTTCA 2040
2041 GGTTCTGCAGATCCCGTTGCGATGCTGTGCACAGCACTGACAGATAAGATTTGACCTTT 2100
2101 CGACTCCGTCTTTGGGGACTTTCCCGCTGGCCAAGAAGGGTAGTTCCAATCCCAGGAAACG 2160
2161 GGCTTCTGCTCAGGAACGCAGCCTCTAGCAGCGCACAGTCTGAGGCAATGTCTCCGGCA 2220
2221 ATTAGAACGATGCTGGGCGCCCGGGTGTGCATCACTCTGCCTCATACTCCTACCAACTGC 2280
2281 AGGGCACTCGGTCCGGCAGCCAGTCCATCCCAACCAAGTCCCAGCCAGCCGGAC 2340
2341 CTTACGCAGGACCCCGATGATAGGTGCTTGACGGCTGCAGCAAAAGCCAAGGCCACCTGC 2400
2401 CGCTGCTGCCCATCCCCGCCAATCTGAGACCCCTAGACTGGACCGCAGAAAAGCGTTTC 2460
2461 TATGGGAACCCCCCACCAGGAATCACGTGACGCAATCGGACGACCAATCGCTTCTTACC 2520
2521 TCTGCCCCGCGGTCCAGCTTTTGGCCCTCCCTCTCGCCCCCGCCTCCTTCGCCCCAGCCCCG 2580
2581 CCCCTTGCTGCGGAGAGCCCGCGCTGCGCGCTGTGTCTGCGCGCTCCTTCCCTCGCG 2640
2641 CGCGCTCTCCGTGGAAGAGCAGGGGCAGCGTGGGAGGCGCCAAGGGAGCGCGAACCTGAG 2700
2701 GAGGAAGAAACGGGGCTAGCGCGCAGGCCAGAACGGTCCGAGCCGCGGCAGTGGCGGAC 2760
2761 GCCTCAGAGCGGAAGAGGGAAGTGAATCAGGCGCCGGGTAGTGGGTTGCTGGGCTGGGCT 2820

2821 TGCTGAGGTAGAGGCAGCGCCAAGAAGAGGCCTTTGCCGCTGGTCGGGATTGGGATGTGCG 2880
M S

2881 AAGAACACAGTGTGCTCGGCCCGCTTCCGGAAGGTGGACGTGGATGAATATGACGAGAAC 2940
K N T V S S A R F R K V D V D E Y D E N

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Fig. 22 (continued; 2/5)

2941 AAGTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCCCGACGAGGGCGAGGTG 3000
K F V D E E D G G D G Q A G P D E G E V

3001 GACTCCTGCCTGCGGCAATATCCTTGCATTACCGCCCTCCCCACCCCAGCCCAGCCCAG 3060
D S C L R Q

3061 CCCGCCCTTCTCCTGGGACCCGGGAGCCTGCAGGATCCGCGGGGCACCGGCGCGGAGCTG 3120
3121 CCTCTCAACCTGCGGCTTAACCTGTCTCTTTGGGATCGCCCGCTCTGAGAGGGCAAGGGG 3180
3181 GAAGCCCCCGTTTCTACCCAGTCGGCAGGAGACGCGAGGGTCCCCTCTTGGGAAGCCTG 3240
3241 CCCTACCCCGCGCGCCTTCCACGCCCCCAGATTCTCAGGTTGCACCCGAGTGCCTGCCT 3300
3301 GCCTCGGGAACCTGGTCCC GCCCGCCCGCGCCCTCGCGGCGCTGGGGAAGGCGGCCCGGCT 3360
3361 GGTGGGGAAGGCTGGTGCCGACCGCCTTAGTTTTTCTTCTAGAACTCTGATTTCTGGG 3420
3421 GTCACATTAGCTCCAGAAATTTCTGATTGTGGGGAACCTGCATCTTCTCTAGTGGTTTT 3480
3481 GTTTTTTGGTTGTGTTTTTGTATTGGTAGCGTTAAGGTAGTTTATTGCTTACCGGGGGG 3540
3541 CCGGGGGAGATGGGACTGTTGCGAAAATTGAGGGTCCCTGTGCTTTCAGCCCATTTGGCCTT 3600
3601 TTTAAAAAAAAAAAAAAAAAAGAAGAAGAAGGGGATTTGGCAAAATATACATTGTACAG 3660
3661 AATTTGTTAACTGGGGGAGGGGAATGAATACAAAAAATACAAAACCTCTAGAAAGGAAGCT 3720
3721 TGGAGCCTTTTACCTGCTAAGAAAAGGACAATAGAAAAACAACGGGGAATGCGTGTGGA 3780
3781 GAATCCTTGGAAATATTTAAATAAACCCCCAATGAATAAGATAGAAGATGAGTCATTCTG 3840
3841 ATAAAGCAGAATCATTTTTGTAATCCTAAAATTGTTCCATTTTAGTTAAATATGGCAG 3900
3901 TCAGTTCCCGGTTTCTGTTTTTGCATATTTGAATATTCATAACTTTGGCTTCGCATTTGC 3960
3961 ATTACATCTTTTTTAGAAAAATGTAATGTTGCAAAAAAACCGAAGCTGTAGTTTAGAA 4020
4021 AATCTCAGACACTGAATTTGTATGCATTTCTAATTTCTGGGTGTATTCAATAAGGAAGACT 4080
4081 CTCAACAATGTCCTGTTATAGTGGGGAAATATGAGAGTGAAAATATTTAATGGCAACAAT 4140
4141 ATCCTTTTTTAAAGGCACCTAAATAGAGCATTAGACATTTATCAATATATAGATAGTGCT 4200
4201 TTGCCCAACTTTACAATTAATTAGCTGTTGCTCTTTTGCATTATTTAAATACTTAAGTG 4260
4261 CTTGGAGTTATAAAAAATGAGCTAATCTACATCAGGCATGCTTCTCTAGAAATCCCTGCA 4320
4321 GCCTTGAAAATAACAGCTTGTCACCAGAGATTTTGTGTAAGAACTTTTTCTTTAGAAAA 4380
4381 TAAATGGTGAACATGCTTCCTAAAAACATTATTTGTGATGGGATAAGATGGTGTTTTATG 4440
4441 AAACCCAGTGATTTTTAGGTAATTTGTGGTGACTTTTAAAAGGTACTGCTGTATCCATA 4500
4501 TCAGTGGATCTGCTTTTTTGATCAGTTCATCTTAAATATAAAGATACTGTCTCTTCTTAC 4560
4561 CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGGTACTAGAGTTGGAGGAACAAG 4620
4621 TGAATCTGTGGTTTTCTTTTTAGGGGAATGTTTGTACATTCTGACAGTCTGATTGGCCT 4680
4681 TCTGTTTCTCATGCTTGCTAACTCACTAGTGCTTTCAAAGAGAGCCTGAATTTAATAGGT 4740
4741 ATGGTCTAACACAGTTTGAATAACCTTTGTGAAATATGAGAGAAAATATCTAAAGCAAAA 4800
4801 AATTAAGCTGCCACCTAAGGGACATATGAATTATTACATCTTCTGTGATGCCTCTTTTCA 4860
4861 TCAATATTGAGAGATTGCTAATGTGTATCATTAGATTGCTAATCTGCCAGCATGTTCTA 4920
4921 CCAGCATTTTCAAGATAATACAGAATATGGTTCTAGCAAAAGTTTGGTCTTTATTTTTTCAA 4980
4981 TTAGAATCACAGGAAAAGACATATTTTGGTTGATAATAGGTTATTTTCAATTTGGGGGACTA 5040
5041 ATAATTCTGATATATATTTTAGGATTTCTTTAACACCACTCTAGGTAATGTTTGCATATG 5100
5101 TATCTCACTGGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG 5160
5161 AAACAGTCTTTGCTTTATTAATAAAAAAGTCTAATGTTCTATTTTCTTTTGTATTTTGC 5220
5221 CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCCAGTATTGAACATAGTGACCAA 5280
5281 AGTAATTTTCTTTTTATATGTAAATCAAGTCATAAAGAACCAGTGGTTATAATGCTTTCT 5340

5341 GGGGGCCATCCTTTGCTGTTACACCCTTAACTTCCATCACAGGAAACATGACAGCTGCCC 5400
G N M T A A L

5401 TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC 5460
Q A A L K N P P I N T K S Q A V K

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Fig. 22 (continued, 3/5)

10023529 "121701

5461	GCAGACTACAACACAGTGATCTCTGCTGATATCTTATTCTTAGTAAAATCCTTGCAGTGC	5520
5521	AAAAAAAAATCAATATTTTAACTGTTTGCTATCTTTGACAAGAAGAGTTTATAATGTAGT	5580
5581	TTGATAGGTAAAAATTTACAGTGAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC	5640
5641	ATGGTAAGATACAGTAAGTTCAAACGATAGTGAAATCATTGTGTGTGTTTTAGAGGAG	5700
5701	ACCACTCAGGCTGAATTTGAGCAAAGGTTTAAAAATAAGTTAAACCTTTACAAAAATAA	5760
5761	ACAGATTGTAATTGCTTTTTTAAAGATTTTTTAAACCATACAAATACTAAATACTTATTA	5820
5821	TAGAAAGCTCAGACATATGAGAAGGTTAAAAAGATAGTGGTTTGTGGTCCCAGCACCCAG	5880
5881	AGATAACAGTTACTACTTTGGGGCCTTGCTGTATTGTTACAGAGTTCCCTTTTGTTTTTT	5940
5941	TAAGAATGAATTTTTTAAACGGGCTTTTTCAGCTATATGCAATGGTACATGAGCTTTCCT	6000
6001	TCCCCAATAAGTTAATAGCCTTTTTTAACTTGTATATGGATAAGCTCCAGTGTATACA	6060
6061	TAATAATCTTTTGTATATTTAGACTGACTTTTTTTTCCATATGTAACCACTGAAA	6120
6121	TCAATATTTTTTGGTAAATTTTTAATTGTTCTCTTTGAGTAAATTGCTAGCAGTGAATTA	6180
6181	CTGGATCAAAGAATGCACTTTTTTTAAGGCTTTTGGTATGCAGTATTGCCAAATTGCC	6240
6241	TTCAGAACAGTTGTGCACTTACATTCTCTGCAGTCTTTACTAATTCTTAACCTATTTA	6300
6301	CGTATTTATTTAAATGATGCCCATAGCATCAACCCGTTGTCCATAGCTATTACATACAT	6360
6361	CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTAATAACTTAGGTAAATGCATA	6420
6421	ATAATTATCTAGGTAACATAATTTTTTATTGGGGAAAATTTCTTTGGTTTTTACAAGTTG	6480
6481	TAAAGATTGTCGTTGAAATTTCAATTTTACCGTGGATGCAAAGATATTTTTCTAAATCTG	6540
6541	GTAATTGCAGTCTTTAAACCAAAGATAACAGTAGGTGGTAGAAACATTCTGTGAAATCCT	6600
6601	GACCAGTAGGAATGCTGGAGGTATCACTTTGTGTTGAATGGAAGGAGAAACGAATTGTTG	6660
6661	AAAAGTCAAGTTAAGTGTTCCTTTGCTTGGCCGGATGGGTAAGAAAATAACTGCTTTTG	6720
6721	AAGCAGGCTTTTGCCAAAGAAAAAGATCATTATTAATGAACATCACTATATTTTATATC	6780
6781	TACAGTCAATTCATATAAATTACAGTCAATTTCTTTAAGACAGCTTGGTTTATTAAAA	6840
6841	TTTTTAAATAAAAAAGTTTTTAAAGAAAAAATTACTTCTGAAGGATAATTCAAGGTGAAAC	6900
6901	TGCAAATCTGCCTCCTTGTGTTTGGGAATTTTTTTTTTTTTTTTTTTTTTTTGGAGACG	6960
6961	GAGTCTCACTCTATCACCCAGTTGGAGTGCAGTGGTGAATCTCAACTCACTGCACCCT	7020
7021	CCGCCTCCCGGGTTAAGCAATCCTCCTGCTTCAGCCTCCCGAGTAGCTGGGATCACAGG	7080
7081	CACACACCACCATGCCTGGATAATTTCTGTATTTTGAAGAAAACAGGGTTTTACCATT	7140
7141	TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCATCTCGGCCCTCCCAA	7200
7201	GTGCTGGGATTACAGCTGTGGGCCACCACACCCGGCCGTTTTGTTGGGATTTTTTTTTTT	7260
7261	TAAGATCAAGACATAAATTTAAATGTTGTTTAAATAAATTGTTAAATTATCACATTGATC	7320
7321	TGTTAGCAAATCCTCTCAGCTCTGCCTTCAATTATGTTAATAGTCTGTCAAGTTTCTTAC	7380
7381	CACCTCCACTGCTACTATGCTTACCACATCCAGCCTGTATTATTGCAATTGCCTCCTAAT	7440
7441	TGCTCTCCCTGCTTCTACCTTATCCCCTACTCCCACAGCTTATTTCTGTAACATAGATG	7500
7501	CCAAAGCAATCCTGTTAAATGTGAGTCAGATTATGGCACTGCTCTTAAACCTTCCAAT	7560
7561	GTCTTCTCATTTCTCTCAGTAAAGCCAACTCCTTACAATGCCTGTAGGCCTTACACGA	7620
7621	TCTGTCTCCCATAACTCTGACTTACTCACGTGCTTTTCTCCCACCAATCCACTCCAAC	7680
7681	CACATTGGGTTTTTTTTCTGTTTCTGGAACACACTGAACACACACTAATAGCACTGTTCTT	7740
7741	TCCTCTGTCTGAAACACTTTCTCAGTTATCCCAAGCCTTCTTTCACGTCTTTCAGGTCC	7800
7801	TTACTCAAATGTCACATTCATAGTGTAGACTTTCTGAAATTCTAAACCCTCCTCATACAG	7860
7861	ATATGTCTAAATGTTCTGTTATTTATTGACCCACCAGGACCGGGCAGGCAGCATTGTCTT	7920
	D R A G S I V L	
7921	GAAGGTGCTCATCTCTTTTTAAAGCTAATGATATAGAAAAGGCAGTTCAATCTCTGGACAA	7980
	K V L I S F K A N D I E K A V Q S L D K	
7981	GAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCGTCTGACAA	8040
	N G V D L L M K Y I Y K G F E S P S D N	
8041	TAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGTAAGTTATGAATTATAAATCTATAT	8100
	S S A M L L Q W H E K	

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Fig. 22 (continued, 4/5)

10023529 "12101

8101	GACTGGTTCTTTTACAATAGGGAATGACAATGACAACCTCTCTCACCTAAATAACCATTT	8160
8161	TGATTTGTTGTACATTTTTGTTATTACAAATAAAATGCATGAAAAGGATAGTTTCATATTT	8220
8221	ATGTTTACTAGCCTTGGTCTTAAGAGATTCTGATTCCAACACTTGTGTTTATTCAACAAT	8280
8281	GATTATTAGTAATTAACATAATCTTGAACCTCTGAATTAAATCAAACTTTGTAAAAGAA	8340
8341	AATAAGCAATACAAATCAAGAATTCCTTCACAGTGACCAAAAGGTGAAAACAACACAAGG	8400
8401	ATCGAATATGATTCAACCA	8419
8420	TTAAAAGGAATGACATTCTGACACATGCTATAACATTAATAAACCTTGAAAACATACCAA	8479
8480	GTGAAATGAGCCAAACACAAAAGAACTAATATTTTATAATTTTACTTATATGAAATAATC	8539
8540	TAGGATAGGCAAACACAAAGGGACAGAAAGTCCCTAGAGGTTACTAGGAAGTAGGGAAAG	8599
8600	CAAGGAATAGGGAGTTAGTGCTTAATAGGTACAGAGTTCCTCCTTGGAGTGGTAAAAAAG	8659
8660	TTTTGGAAACAGATAGTGGTGATGGCTACAGTACATTGTGAATATAATTAATGCCAATGG	8719
8720	ATTTTACACTTAAAGATGGTTAAAATGGCAAATTTTGTGTTAGATATTTTACAACCTTTT	8779
8780	TAAAGAATTAGGAGTTTGGAGGATCAAGAATTCCTTAAATCATGTTTTTCTATTTTCATGT	8839
8840	GTATATTTTGCAATGTAAGTAGATGCTGGTACATCATCTGTCAAAAGAGTATAAGTGATT	8899
8900	TTGAGCTTTGGGTAAAAAAGTGGATAACATGTAAATAGAACCAGTCATAAAAAATATTGAG	8959
8960	TGTTTGAAGTGTATCTGAGTGAAAACACAAACATAAGAAAAAAGCACATAGTAAAAACAAT	9019
9020	AGTTCCCCCTTTTACTCTAAAATGCACCAATTTGGGTAGTAATTTATATGGCACCCCTATT	9079
9080	CATGGAACACTTTCTGTTGCCAGGTACCATACTATTAATGTTTTATTTAACCTTTACAAC	9139
9140	AACCCTGTGGAAGTATATAAATATCTTTATCATCCTCAATTTACAGATGAAAAGCTAGCT	9199
9200	TTAAACCCCAAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCAGTGAACATTGATTAC	9259
9260	TTATTATATTCCACATATTCTTCAAAGGACTTTATAAATATTAACCTATTTAATCCCTCAT	9319
9320	AAAAATGGAGGGAAATGCTTCTGCTATTATTCCTCTTTTGTCACTGAGGAAACTGAGGCATG	9379
9380	TGTGAAGTCTTCATTTCTTCCAATGTCAAGTACCAGTTTTTACCAATCTTCGAAGTATT	9439
9440	TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTTACAGCATCTCTCCAGTCT	9499
9500	GTTGCCATAGCTTCCCTGACTGGTTTCCCAGTTAACAGTTTTGCCTCCTTCAAATCTGTTT	9559
9560	TCCACCCAGCCATCAAAATGATATCTTTAAATCAAAATTGCCCTTGTCAGTCACCTGCA	9619
9620	GGGATAAAGTCAAAGTTCCCAAGTCTAGCTTCATCTCCATGTCATTCTTCCCCTCAGGC	9679
9680	TATAGCAATGCCAGCCTTTTTCTGAATGCACCATATTGTTTCACACCTCCATACATTTG	9739
9740	CTCATGATTTTCTGGTGTTAGCCTGTCACTACTCATTCTTTTAATGTGTCAATTCCTCC	9799
9800	ATGAAGCCTTAGCTGAAACATTCTCTATACTGTTAATCTGGGTATAAGCCTCTCCCTGG	9859
9860	TGCTTTAATAGCACCTGCAGCACAACTCTCATTTTCATACATTAGATTAAAATTACCTGTT	9919
9920	TATATGTCTGTCTCCTCATGCTAGACCAGAAAATGCTGTATTTGTTCACTTTTGTATCCC	9979
9980	CAGCATCTAGCACAGTACTCAGTATACAAAGGTATTCCATAAATATTTTTTGAACAGAAA	10039
10040	GAAACCAGAGCTCAGATTCCATAACTTGATCATTACTCTCTATTTTTTCAAATTAGAGTC	10099
10100	AGAGTTAAAGTTTCTAAGTTCTTAGCTATTAACAATAACCTTCTTTCTTTGGGAGAAAAA	10159
10160	AAATCTGACAAAGGCTGACTAATCGAAGTGGAAGTTGGGATGGTTGATCCCAGTTTGAAT	10219
10220	TTTCTTCTGACTATGTGGTGAGAATGAGAAATGTCAGAATGTCCACCTGTTTTGAGCAGGA	10279
10280	ACACTATGCTGCAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTTGC	10339
10340	TCTGTCGCCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCTCCT	10399
10400	GGGTTACACACCATTGTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCA	10459
10460	CCACGCCCCGCTAATTTTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTAGCCAGG	10519
10520	ATGGTCTTGATCTCCTGACCTCGTGATCCGCCGGCCTCGGCCTCCCAAAGTGCTGGGATT	10579
10580	ACAGGCGTGAGCCACCGCGCCCGGCTATGCTGCAGATTTTTTAAAACATTATTTAGAAT	10639
10640	TAATGTACTAAAATGTAACTAGTATCTCACTAGAATGTAACCTCATGAGGGCAGGGACT	10699
10700	TTCAAGGTTTTGTTTATTACTGTAACCTCAGTGCCAAGAACAGTACCTGGTGCATAATTG	10759
10760	GTGCTCAAGAATTTATTATTTGTTAACTAATAAATTCAGGGTCTATAGCAGTGCCCATTC	10819
10820	CTTCTTTAAGAAAAATGTTTTTACCAAATATGAGAATTGACCTTTTATTATTCTGTCAACA	10879
10880	TTTACATCCTGGTTTGTTTTTTAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTTCTGTG	10939
	A L A A G G V G S I V R V	
10940	TCTTGACTGCAAGAAAAAGTGTGTAGTCTGGCAGGAAGTGGAATTATCTGCCTCGGGAGTG	10999
	L T A R K T V *	

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Fig. 22 (continued, 5/5)

11000	GGAATTGCTGGTACAAAGACCAAAACAACCAATGCCACCGCTGCCCTGTGGGTAGCATC	11059
11060	TGTTTCTCTCAGCTTTGCCTTCTTGCTTTTTCATATCTGTAAAGAAAAAATTACATATC	11119
11120	AGTTGTCCTTTAATGAAAATTGGGATAATATAGAAGAAATTGTGTTAAAAATAGAAGTGTT	11179
11180	TCATCCTTTCAAACCATTTTCAGTGATGTTTATACCAATCTGTATATAGTATAATTTACA	11239
11240	TTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTT	11299
11300	TGTATTATTTTAACTAATACTGAGAGATTGGTCAGAATTTGAGGCCAGTTTCCTAGCT	11359
11360	CATTGCTAGTCAGGGAAATGATATTTATAAAAAATATGAGAGACTGGCAGCTATTAACAT	11419
11420	TGCAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATATGTTTTTGAATAAGTGG	11479
11480	TGGGTGAATACCACTGCTAAGTTATAGCTTTGTTTTTGCTTGCCCTCCTGATTATCTGTAC	11539
11540	TGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCCTCAATTTATT	11599
11600	TGTGGTCACCCAGGGTTCAGAGCAAGAAGTCTTGCTTTTATACAAATGTATCCATAAAATA	11659
11660	TCAGAGCTTGTTGGGCATGAACATCAAACCTTTTGTTCCACTAATATGGCTCTGTTTGGAA	11719
11720	AAAAC TGCAATCAGAAAGAATGATTTGCAGAAAGAAAGAAAAACTATGGTGTAATTTAA	11779
11780	ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTTAGA	11839
11840	CATTATGAGGTATACAAC TAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTC	11899
11900	AGTGTTCTTCAGGGTAGTTGGGATCTCAAAGATTTGGTTCAGATCCAAACAAATACACA	11959
11960	TTCTGTGTTTTAGCTCAGTGTTTTCTAAAAAAGAACTGCCACACAGCAAAAAATTGTT	12019
12020	TACTTTGTTGGACAAACCAATCAGTTCTCAAAAAATGACCGGTGCTTATAAAAAGTTAT	12079
12080	AAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCTTAG	12139
12140	TATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATT	12199
12200	CTATAAACTCTTTGCTGTTTTTGATACCTGCTTTTTGTTTTCATTTTGTGTTTTGTAA	12259
12260	AAATGATAAACTTCAGAAAATAAAATGTCAGTGTTGAATAATTTATTTTTCTCTGACAC	12319
12320	TTTAACAATTATGAATGTATGGTTAATTAAGAGGAAAGGTTTTCTGCTTCTACCACCAAG	12379
12380	TACTGTACTCTTAACAAGAACAGTTTGGTAGGGTTTTTATAAGACTATATAGATATAAGA	12439
12440	TGATAGAGAAGAGAGTCATGAATGATGTCAGAGCACTACTGAAGCCTTTGGAGTGATTCC	12499
12500	ATAGCCTTCTGGATGGCAGCTGAATACCTATATGTAGTATCACTGCCCAAAGACCTAGAC	12559
12560	TAGAAAGTGCAAAGTAGCTTAGCAGCTGCAGTCATTCCTCCAGCCTCCAAAATTCTCT	12619

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Fig. 23 (1/6)

1 - GATCCCTCTCCAGGTGGAAG - 60 /|\
61 - CTCCCTTCATACCAAAGTTTAAAGGCCCTGGGGATACGAGTAACTTTGACGACTATGAGG - 120 |
121 - AAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTTCTGAGTTTTAGG - 180 |
181 - GGCATGCCTGTGCCCCCATGGGTTTTCTTTTTCTTTTTCTTTTTTTGGTCGGGGGGG - 240 |
241 - TGGGAGGGTTGGATTGAACAGCCAGAGGGCCCCAGAGTTCTTGTCATCTAATTTACCCC - 300 |
301 - CACCCACCCCTCCAGGGTTAGGGGGAGCAGGAAGCCAGATAATCAGAGGGACAGAAACA - 360 |
361 - CCAGCTGCTCCCCCTCATCCCCTTACCCTCTGCCCCCTCTCCCACTTTTCCCTTCCTC - 420 |
421 - TTTCCCCACAGCCCCCAGCCCCCTCAGCCCTCCCAGCCCACTTCTGCCTGTTTTAAACGA - 480 |
481 - GTTCTCAACTCCAGTCAGACCAGGTCTTGCTGGTGTATCCAGGGACAGGGTATGGAAG - 540 |
541 - AGGGGCTCACGCTTAAGTCCAGCCCCCACCACACCCCATCCCAACCAACAGGCC - 600 |

Human cAMP-dependent protein kinase
catalytic subunit alpha

Accession number X07767 (until *)

- follow arrow until line that
begins 1561 -

601 - CACTTGCTAAGGGCAAATGAACGAAGCGCCAACCTTCCTTTCGGAGTAATCCTGCCTGGG - 660 |
661 - AAGGAGAGATTTTGTAGTACATGTTCAAGTGGGTTGCTTGCTAGATTTTTTAAAAAAC - 720 |
721 - AACAAATTTAAATCTTATTTAAGTTCACCAAGTGCCTCCCTCCCTCCTCTACTCCC - 780 |
781 - ACCCTCCCATGTCCCCCATTCCTCAAATCCATTTTAAAGAGAAGCAGACTGACTTTGG - 840 |
841 - AAAGGGAGGCGCTGGGGTTGAACCTCCCCGCTGCTAATCTCCCTGGGCCCTCCCCGG - 900 |
901 - GGAATCCTCTCTGCCAATCCTGCGAGGGTCTAGGCCCTTTAGGAAGCCTCCGCTCCTT - 960 |
961 - TTTCCCAACAGACCTGTCTTACCCTTGGGCTTTGAAAGCCAGACAAAGCAGCTGCCCC - 1020 |
1021 - TCTCCCTGCCAAGAGGAGTCAATCCCCAAAAAGACAGAGGGGGAGCCCCAAGCCCAAGT - 1080 |
1081 - CTTTCTCCAGCAGCGTTTCCCCCAACTCCTTAATTTTATTCTCCGCTAGATTTTAAAC - 1140 |
1141 - GTCCAGCCTTCCCTCAGCTGAGTGGGAGGGCATCCCTGCAAAAGGGAACAGAAGAGGCC - 1200 |
1201 - AAGTCCCCCAAGCCACGGCCCGGGGTTCAAGGCTAGAGCTGCTGGGGAGGGGCTGCCTG - 1260 |
1261 - TTTTACTCACCCACAGCTTCCGCTCCCCCATCTGGGCGCCCTCCTCCAGCTTAGCT - 1320 |
1321 - GTCAGCTGTCCATCACCTCTCCCCACTTTCTCATTGTGCTTTTTTCTCTCGTAATAGA - 1380 |
1381 - AAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCGTATTTCCCCCTCTCATACT - 1440 |
1441 - TCTCCCATCCCAGGAGGAGTCTCAGGCCTGGGGTGGGGCCCCGGGTGGGTGCGGGGGC - 1500 |
1501 - GATTCAACCTGTGTGCTGCGAAGGACGAGACTTCTCTTGAACAGTGTGCTGTTGTAAAC - 1560 |
1561 - ATATTTGAAAATATTACCAATAAAGTTTGT*TAAGGAGGAGTGTGCTGGTGTCTC - 1620 |
1621 - GACTTCGATCACCCACCCACACACCCCAAGGGGTTGGAAAGGGAATTCGACCCACAGC - 1680 |
1681 - GTGCAGGCCGATCAGGTCTGGCTTGAAGTCTTGTAAACAGGGTTAGCTGAAATTCGG - 1740 |
1741 - GCACTCCTTCGGCCCCGAGGAGAAACGAGCGTCAAACTGCCCTTTGACCCAGATTCGG - 1800 |
1801 - GGTCCCAAAATCTGCGGCGCGCCCCCTCGGCGTCCAGCCGGGACCGAGAGGGCGCTCTA - 1860 |
1861 - GGGAGGCGCTGGGGCTGGCGCGCCAGGAGGCCGAGCGGCGGGGGCGGCCCTGGCAGG - 1920 |
1921 - GGGAGTAGAAGGGGGAGAGGGTGCAGCCCCCTTCCCGCATCCTCAGCGCCGGGCCAGG - 1980 |
1981 - CGCGCTGAGGGACGCGGGGGCGGCGGAGTTCCTGGTAAGTGGGTCCCGAGAGCGGAGCGC - 2040 |
2041 - CGGCAGCCCCGCGCGGGCGGCGAGTTCCCGGTAAGTGGGTCCCGAGAGCGGAGCGC - 2100 |
2101 - GCTGGAGAGGCGTGGAGAGGGGGGCTGGGCGCGGGGACGTCTGGGTCCCGCGCCCAATG - 2160 |
2161 - GCTGGAGGGCGGCGGAGCGCGCGCCCGCCCTGCCGCCCCCTCTCCCTCCCCCGGG - 2220 |
2221 - CACTCCCTCCCCCTCCCCCGCCCGCGCTTTCCCCCGCCCCCGCCCGGCGCCAATCC - 2280 |
2281 - GCGGCGCTCCTTAAAAAGCGCGGGGAGTTGTAAGGGGGGGCGGAGCGAGCCGGAGTG - 2340 |
2341 - AGCGAGAGCGCAGGGTAAAGGGGGCGGGCGGGGGGCCGGGCTCCACCTTAAAGCGGGC - 2400 |
2401 - GCGTGGGGGTGGGAGGGAGGAAGCGGGCGGGGAGGAGGGAGGGAGGAAGGAAGGG - 2460 |
2461 - GGGCCGAGTGTCCCGGGCGAGGGCGCGCGTGCAGCGGGCGGCGGCGGGGAGGGGCC - 2520 |
2521 - GGCCGCGCGCGCTCCCTCCTCCCCCTCGCATCCCCGCCCCGCGCGCGCCAGAGAA - 2580 |
2581 - GCGGGTCTGTGTGCTGCGTGCAGTGTGAGTGTGTCATATTTTTTCTCTCTTTT - 2640 |
2641 - TCTTTCTCTCTCACTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTTTTTTTTTT - 2700 |
2701 - TTTTTTTTTTGAAAGAAACAGCAGCGCGCGCCGCTCCGCGAGGCGCTGCGCCCCC - 2760 |
2761 - GGGGGGGAGGCGGAGGAGCGGGCAGCGCGGAGGGAGGGGAGGGGGAGGGGGCGC - 2820 |

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fig. 23 (continued, 2/6)

2821 - CGCGCTGGGAGGGAGGCAGCGCGCACGGTGCAGCCGGGCGGGCGGGAGGCATGGCGGGG - 2880
- M A G

2881 - CCCCCGGCCCTACCCCCCGCGGAGACGGCGGGCGGCCACCACGGCGGCCGCCCTCG - 2940
- P P A L P P P E T A A A A T T A A A A S

2941 - TCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGACTCGCTGCGC - 3000
- S S A A S P H Y Q E W I L D T I D S L R

3001 - TCGCGCAAGGCGCGGCCGACCTGGAGCGCATCTGCCGGATGGTGGCGGCGGCGGCACGGC - 3060
- S R K A R P D L E R I C R M V R R R H G

3061 - CCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAACTGATCCAGCAGCGCGCCGTGCTC - 3120
- P E P E R T R A E L E K L I Q Q R A V L

3121 - CGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGTCCAGCCGCCCGG - 3180
- R V S Y K G S I S Y R N A A R V Q P P R

3181 - CGCGGAGCCACCCCGCCGCGCCCGCGCGCGCCCCCGGGGCCCCCGCCGCCGCCGCC - 3240
- R G A T P P A P P R A P R G A P A A A A

3241 - GCCGCCGCGCGCGCCCGCCACGCCCGCCCGCGCCACCGCCCGCGCCCGTCGCCGCCGCC - 3300
- A A A P P P T P A P P P P P A P V A A A

3301 - GCCCCGGCCCGGGCGCCCCGCGCGCCCGCCCGCCCGCCACAGCGCCCCCTCGCCTGGC - 3360
- A P A R A P R A A A A A T A P P S P G

3361 - CCCGCGAGCCGGGCCCCCGCGCGCAGCGGGCGCGCCCTGGCCGCGCCGCCGCCCGCG - 3420
- P A Q P G P R A Q R A A P L A A P P P A

3421 - CCAGCCGCTCCCCCGCGGTGGCGCCCCCGCGCGCCCGCGCGCCCCCGCCGCCGCC - 3480
- P A A P P A V A P P A G P R R A P P P A

3481 - GTCGCCGCCGGGAGCCGCGCTGCCGCGCCGCCACAGCCCGCGCGCCGCCACAGCAG - 3540
- V A A R E P P L P P P P Q P P A P P Q Q

3541 - CAGCAGCCGCCCGCCCGCAGCCACAGCCCGCCCGGAGGGGGCGCGGTGCGGGCCGGC - 3600
- Q Q P P P P Q P Q P P P E G G A V R A G

3601 - GGCGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGCAGCGGCGGC - 3660
- G A A R P V S L R E V V R Y L G G S G G

3661 - GCCGGCGGTGCGCTAACCCGCGGCCGCGTGACGGGGCTGCTGGAGGAGGAGGCGGCGGCT - 3720
- A G G R L T R G R V Q G L L E E E A A A

3721 - CGAGGCCGTCTGGAGCGCACCCGTCTCGGAGCGCTTGCGCTGCCCCGCGGGGACAGGCCC - 3780
- R G R L E R T R L G A L A L P R G D R P

3781 - GGACGGGCGCGCCCGGCCAGCGCCCGCCGCTCTCGCAGCAAGGTGAGCGCGCCGGGG - 3840
- G R A P P A A S A R P S R S K

3841 - AGCGGGGGCGCCGCGCGGTGGGCAGGTGCGGGCGAAGTTGGTGGCGGGGGCGGAGTCCC - 3900

3901 - GGGAGGAAGTGGGTGGCGGCTGGCTGGGGCTTTGCGCGCGTTTCTGCGGGCTCGGTGCG - 3960

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Fig. 23 (continued; 3/6)

3961 - TGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTCCTCCGCTGTAAACGCG - 4020
4021 - GTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGATTTGGTTGTC - 4080
4081 - GAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTAGTCCGTATT - 4140
4141 - GTTCTTAAAGGTGGAATCGGTTCTCTCTCCCCACCGCCCGGACGCCACAGTCAGGGTCTG - 4200

4201 - GGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCTCCTCGGCTCCAGAGAGGTGGAGAAG - 4260
- R G G E E

4261 - AGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATG - 4320
- R V L E K E E E E D D D E D E E D D

4321 - ATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCACCACC - 4380
- V S E G S E V P E S D R P A G A Q H H Q

4381 - AGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCT - 4440
- L N G E R G P Q S A K E R V K E W T P C

4441 - GCGGACCGCACCAGGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGCAGCGGCACCCGCC - 4500
- G P H Q G Q D E G R G P A P G S G T R Q

1 - AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAACAGGTAAGGATCCCTCTGGGT - 60
- V F S M A A M N K E G G T

61 - GGGGAAGAGTGCTAGGTGGAGAGGAACCTCAGCCCGAAGACAAAGCCAAAGACAGGTGTTT - 120

121 - TTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCGTGCCTTTGCCC - 180
- A S V A T G P D S P S P V P L P

181 - CCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCTTTGGCTGTCCGTAAGTTGGG - 240
- P G K P A L P G A D G T P F G C P

241 - GTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCGTGTT - 300

301 - CACTGGTGTCTGTTTGTGTTTGGATGCAGTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGT - 360
- P G R K E K P S D P V

361 - CGAGTGGACCGTGATGGATGTGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGC - 420
- E W T V M D V V E Y F T E A G F P E Q A

421 - GACAGCTTTCCAAGAGCAGGTGAGTTTCCAGCCCAGGACTACACACTGACAGACACAGAG - 480
- T A F Q E Q

481 - GGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTTCTGTCCACCCAGGAAATT - 540
- E I

541 - GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 600
- D G K S L L L M Q R T D V L T G L S I R

601 - CTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT - 660
- L G P A L K I Y E H H I K V L Q Q G H F

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Fig. 23 (continued; 4/6)

661 - GAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCAGCCTCACCCCTGCCCCAGCC - 720
- E D D D P D G F L G *

721 - CATTCCGGCCCCCATCTCACCCAAGATCCCCCAGAGTCCAGGAGCTGGACGGGGACACCC - 780
781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCCTCTTGTCTTATCTTTGCCCTTG - 840
841 - TGTCTGTCTCACACACATCTGCTCCTCAGCACGTGCGGTGTTGGGGAGGGGATTGCTCCTTA - 900
901 - AACCCAGGTGGCTGACCCCTCCCCACCCAGTCCAGGACATTTTAGGAAAAAAAAAATGAA - 960
961 - ATGTGGGGGGCTTCTCATCTCCCCAAGATCCTCTTCCGTTCCAGCCAGATGTTTCTGTAT - 1020
1021 - AAATGTTTGGATCTGCCTGTTTATTTTGGTGGGTGGTCTTTCTCCCTCCCTACCACCC - 1080
1081 - ATGCCCCCTTCTCAGTCTGCCCCCTGGCCTCCAGCCCCCTAGGGGACTAGCTGGGTTGGGG - 1140
1141 - TTCTCGGGCCTTTTCTCTCTCCCTTTTTCTTTCTGTTGATTGTGCTCCAGCTGGCTG - 1200
1201 - TATTGCTTTTAAATATTGCACCGAAGGTTTTTAAATAAAATTTTAAAAAAGAAAAAGG - 1260
1261 - GAAAAAAGCCACGGAGTCCATTTTATGAATGGGGTGGGGAGAGGGCACTAAAGAGCCT - 1320
1321 - CCTAAGAGAGCCTCAGGTTAGGACAGAATTGTTTGGGGAGGGAGAAAAACAGAAACAATG - 1380
1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATTT - 1440
1441 - GCTTTTTTTCTTCTGTAATCTCACCGTGTCCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500
1501 - AGGTGCTCAATTTTGTGTTTTCGTTTAGACAGGTTTCATTCTTTCACCCAGGCTGGAGTG - 1560
1561 - CAGTGGTGCTATCATAGCTCATTGTAGCCTCAAACCTCCTGGGCTGAAGTGATCTCCAC - 1620
1621 - CTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCACTCTGCCATGCCGGGCTAACTTTTAA - 1680
1681 - AAATTTTGTCCGGGCACAGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGG - 1740
1741 - TGGGTGGATCATGAGGTGAGGAGTTCAAGATCAGCCTGGCCAAGATGATGAAACCCTGTC - 1800
1801 - TCTACTAAAAATATAAAAAAAATTAGCTGGGCGTGGTGGTGGTGCCTGTAATCCTAGC - 1860
1861 - TATTCAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGCAGTGAGCC - 1920
1921 - AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCTGTCTCAAAAAAAAA - 1980
1981 - TCTTTGTGTGTGTGTGGAGATGAGGGTATGCACTTTGTTGGCCAGGTTGGCCTCGAACTC - 2040
2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACCATGCCTGGCCTCAAATAT - 2100
2101 - TGTTGAATGGCTAGCAGTTAAGTCCTTGGGTTTATAAGCATTTCCTCAACTGTCTCCCA - 2160
2161 - AGTCCCCATAAGACAAAAAACTCATAAAATCCCACCTTACAGAAGAGGCAGCTGGCCCGG - 2220
2221 - CACAGAGATGCTGTCTGCCCCGGGTACACAGGGTGGCATCTGACACCCTGTCTGAGTTC - 2280
2281 - TTCACTCAGAGTCTTTAAATATAATTAGCGTATTTGACATAATGTACATTAAAAACTATA - 2340
2341 - AACCTGTGAGCCTTTGTCTACTGCAAAGAATCCACTACAAATATTGGGGCAGGGATCTGT - 2400
2401 - TCTTGACCATAGTAGTGTCTCCAGACCTCATGGTCTCTTCATTAAAAACAACAGAAAT - 2460
2461 - TCCTTCTGGGCCATCAGATGAGACCATGAGATAGAAGATTTCCAAGTGAAGATTTGTTT - 2520
2521 - CAAGACAGAGTCTTGCTCTGTCACTCAGGCTAGAGTGTAAGTGGTGAATCATAACTGTGG - 2580
2581 - TGACAGCCTCGAACTTTTGGGTACAAGTGATTCTCATGCCCTCAGACAACACCCAATAAT - 2640
2641 - ATTTTGGTTTTTGTATAGACAGGGTCTTGCTATGTGGCTTAGGCTGGTCTTGAACCTCTG - 2700
2701 - GCCTCAAGCAGTCCTCCCGCTTCAGCCTCCTAAAGTGTGAGGATTACAGACATGAGCCAC - 2760
2761 - CAAGTCCAGCCTGAAGATTTTTTAAAAATATTGTTAGTAGTAGTCGCCAGAGTTACTACA - 2820
2821 - TCCAAAGTCCCTACTAAGTTCTAAGTAGTCCCTACTAAGTTCTAAGGCAGTTTCTCAACT - 2880
2881 - CATTAGAGTTGTTTTTGTGTTTTTAAAGAAAAAAGAGGCTGGGCACTTTAGGAGACCGAC - 2940
2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTTGGAGCAACCTGGGCAACATGGGCCCCCATC - 3000
3001 - TCTAAAAATTTTAAATTAATAAAATGTTTTAACAACAAAAAGCGTTCTGGGAGTGAGGGG - 3060
3061 - CTGGGGCCTGGGCGGCCTCATTCCATATACCTGTGCCGGGTTGAGGGGTTGGAGACACGT - 3120
3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAAGGTCCCGGCCCTAGCCAC - 3180
3181 - ACCCCCAGGACACGGCCAGAGGCCACCTCCCTAGGCGGGTCCCTCCCCACCGCCAGGTTT - 3240
3241 - CTGGAGCGCGTGCGGCGCGTGTGCAGGGGTAGGGGGCCGCGAGGCGCGCGGACTGGAGAGG - 3300
3301 - CGCGCCCCCTCCCGCGTGTGAAATTCAAAGAGGGCGAACGGCCCCCGGCGCGGCGCGG - 3360
3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGGCCAGTCCGAGGCTCCCGGGGCGGGTTCGAACCC - 3420
3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGCTCAGGTTCCCGCCCCCGGCCCTA - 3480
3481 - CCATGGCTACAGAGCAGTGGTTCGAGGGGTGCTCCCCCTGGACCCTGGAGAAACACCGC - 3540
3541 - CTCCAGACGCCTTGGAACTGGGACGCCGCCCTGCGGAGACCCCTCCAGGTCGACGCCCC - 3600
3601 - CTGGCAGGCCTGGGAACCATCTGAGCCGATCCTGAAGATGCCGAGGGGCGGCTGGCTG - 3660
3661 - AGGCCCCGGGCCTCCACGTCTCCCCCAAACCTCTGGTCCCCCGGCCTGGGCCAGCACCTC - 3720

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Fig. 23 (continued, 5/6)

3721 - CCCGCCTATCCCTGGACACTTTGTTTCAGCCCCATCACCCAACAGCTGCGCTACCTACTGA - 3780
3781 - AGAAGGCAGATGATTTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG - 3840
3841 - TCCCCATGGGTAAGGAGACTTGGAGGGGAGGCGACAGGATGGGTGACACACACCAGGGTC - 3900
3901 - GCAAAATTACAAGCGCTAGGAGCCAGAGGGGAGACAGTGGGAAGAAGCTAGCATATTAGAAT - 3960
3961 - CCAGTTTAAAGAGAATGAGGAAGACTGTAGAATTGCGGGTAGGGGATGGCTGCTATTACTG - 4020
4021 - TCGTGGCAGGGTGGGCTGGGGTGTCAAGTCTCTAGGACTTTTTCTCCAGTTTTTAAG - 4080
4081 - TGCTGTCTTACATTTTGAGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAAACTTGG - 4140
4141 - CCTGCAGGACATCAGTTTGAGACTCCAAAGGATAATGTGATTCCCAGACCAGGTTTCCCT - 4200
4201 - GTGACTCTCAATTTAGTGTCCATTGGAATTTCTAGGAGGCTGGGTTGGGTTTGTTC - 4260
4261 - GTGTTTGTGTTTGGAGATGGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCAGTGGTGCAAT - 4320
4321 - CTCAGCTCACTGCAACCTCCGCTCCCGGATGAAGCAATTCTCTGCCTCAGCCTCCCGA - 4380
4381 - GTAGCTGGGATTACAGGCGCCCAACATGTGTTGCCCCGCTAATTTTTTCTTTTCTT - 4440
4441 - AGTAGAGACAGAGTTTACCATCTTGCCAGACTGGTCTTGAGTCTCTGACCTCATGATC - 4500
4501 - CACCCGCTTGGCCTCCCAAAGTGCTGGAATTACAGACGTGAGCCACCGCGCTACCCGA - 4560
4561 - GGCTGGGTTTTTTTGTGTTTGTGTTTGTGTTATGTGTTTTTTTGAATGGAGTCTTGCTCT - 4620
4621 - GTCACCTAGGCTGGAGTGCAGTGGGGCGAACTCAGCTCACTGCAACCTCCGCTCCAGG - 4680
4681 - TTCGAGGGATTCTCATGAGGCTGTTTTTTTTTTTTTAATGAGACAGGGTCTCGCTCTGTC - 4740
4741 - ACCCAAGCTGGAGTGCAAGTGGGGCAGTCATAGCTCACTGCACCCTCGAACTCCTGGTCT - 4800
4801 - CAAGCAATCTTCCACCTCCCTCCTGGGTAAGTGGGACTACAGGTGCCACCATGCCAGC - 4860
4861 - TAATTATTTTTGTGTAGAGATGGGTTCTTGCTATGTTGCCTAGGCTTGTCTGGAACCTCT - 4920
4921 - GGCTCAAGCAATCCTCCAGCCTCAGCCTCCCAAAGTCTAGGATTGCAGGCGTGAGCCA - 4980
4981 - CTGTGCCCAGACCCTGCAGGAAGCTCTGGGTCTAAGTGTGACACTCAGGTGTCAGC - 5040
5041 - ACTTTAAACAAGTGTTCCAAATGGGTTTGTATGCAGGTAAACCAGAAAGATGTTTCAGAAAAG - 5100
5101 - ACCTGAAACTGGGGGCTTTTCTAATGGGTCAAAGCCAGGGATACAGGTGGGATTGAGTA - 5160
5161 - GAATGGGGAAAAGTGCAGGGTGGGGAGGGGTTGTGAGGGATTCCAGGCAAAGGCCCTT - 5220
5221 - CTTCTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGGCCAAGGCCATGCCACCTTCT - 5280
5281 - TACAGATGTGTAGCCCTACTTCTGTACCTGGAGGCAGCCGCGAGAAGCATACCCCCCA - 5340
5341 - TCTATGGAGCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGTGGAGGTTTCTTAGACCCCA - 5400
5401 - CGCCCTTTCTTCTCGCAGCTCTGAGCCTGTGGGATGGTGGAGGGGAGGCCCCACTCCT - 5460
5461 - CGCAGGCCAGCTGATCTCACTGTACCCCTCTTGATGACAGCTGTTAGAGATCTCCCAA - 5520
5521 - CAGCTGACCCTGCGCCTGGAACAGCTGGTCTCATGTACGCTTCTTTGGGTTCTGTTGAC - 5580
5581 - CTGGAGGAGATGAACCCCTTAGGTAAGTGGTAGGAGACTCAGATGGGGGGATGAAGGA - 5640
5641 - GTCCAAGGCCAGCCTCACCCTCCATTCTCTCATGTCTCGCCAGCATCTCCTGTTTCTT - 5700
5701 - TTGCGGGAGGTTCTCCATCAGCCTGTCCCATGAGGTCTCCATCTTCAGATACTGTGCCCC - 5760
5761 - AACCCTTACACTGCCAGCCGCTTCCCCCGCTACCTCTATAAGAAGATGCGCTGGCACCT - 5820
5821 - GGAAGCCACCCAGAGGCCCTGGTGGGGACAAGATTCCCTTGTGGATTAGTAAGTCCT - 5880
5881 - CTTACCCAAATCAAAGTCTCCCTTTCTATGATGAATGCCAATATGACCCTCCAAACCG - 5940
5941 - TCACCAGCAAAGTGAAAAGTGAGCCAGGGCCGAGGCAGTGGCTCACGCCTGTAATCCCA - 6000
6001 - ACACTTTGGGAGGCCGAGGCAGGAGGATCACTTGAGCTCAAGAGTTTGGATCAGCCTGG - 6060
6061 - GCAAGATGGCAAGACCCTGTCTCAACAACAAGAAATTCGCCAGGCGTGATGGCTGGCAC - 6120
6121 - CTGTAGTCCCAGCTACTTGGGAGGCTTAGGCAGGAGGAGCACTTGAGCCAGGAATCAAG - 6180
6181 - GCTACGGTGAGCTGTGATTGTGCCACTGCACTCCACCCTGAGTGGAAAGCAATAATCTGTC - 6240
6241 - TCTTAAAAAAAAAAAAAGTGAACCAGGAACTAAAGGCTTTTGAAGGCTACCTCTATT - 6300
6301 - TTCTTAAACCCACCCTCCACCAAAATAAAAGTTCTCATCTTAAAGTAGGCTGGCAGG - 6360
6361 - GAGAAAAGCCCTGGAGTCACATTCTTACCTGAGAACTTCAAGGCAACTTCTGATGAGTT - 6420
6421 - CCCCACTCACTCCAAATTAAGCCCTCAACAGAACTAGCTAGGAAGCTGATCACTTCT - 6480
6481 - AATTACAGCTCCCTCCCTCTAGCTACTTTCTGTGCTATCGAGATACTTGGGAAGACAC - 6540
6541 - AGGCCAGAGTCCAGCCAATTGCTGCCACAGATCCAGAAGCTGTGGTCCATCGGCCGATG - 6600
6601 - GGTGCCCTTAGGACCAGCCGAGGATGACCTTTATTCATGGTAGGAGCTAGGGCAATAGCA - 6660
6661 - ACGTGGGCTGGGAGCTGGAGGGGGAGGCAGAACCCACCAAAGACAATCCACCTTCCCA - 6720
6721 - AACACTTTGCTTCCCTTAGTAGTGATAGCATTTTATTGTGCCCTGAAAAGCACTTCATGC - 6780
6781 - AGACCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCATTTAACAAAGAAAACAG - 6840
6841 - GGTGCTCAGAGAAGTTGTTACCTGCCCAAGGACACACAGCTAGCAGAGCGAATGGACAGG - 6900
6901 - TCAGGACCAGTTATTACGCTCTAGGAGCCATTACTAAGTCTCTGATCAACAAGGAAAACA - 6960
6961 - AGTTTCCCCCGGGGTTTTTCCCACCCGAGCTGAAACAAAGCCTTTTCACCTGAGCCT - 7020

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Fig. 23 (Continued, 6/6)

7021 - CTCACTCAAAGGGAGGGACTCCCGAGGGGCGAGGGGGCACTCAAGTCCAGGCCTGTCTATC - 7080
7081 - CCTGGCCCCCCCCACCCAGGATTTTGTGCCCCGACCGCTTGGGGACTACCAGCAGCTGCT - 7140
7141 - GACCATCGGCTTCGAGGAGCCCCACGCCCACGCTGGCCACCGACCTGCTGGTGCAGATCCT - 7200
7201 - CACGGGCCAGGCAGGCCAGGCCCGGCCTCCGAGCGCAGCCGGGCCTGCGGGGTGGGCAGC - 7260
7261 - GCAGGGGTCTTGAACCTGGGGAAGAGGGTAGGAGCTGGAACCTGACAGTTCCAACTCCA - 7320
7321 - GAATAGGGGGCAGGGGAGGGGCTCACTCGTTCTCGCAGTGCAGCCGGGCCTCGCCTTCCA - 7380
7381 - AAGGGCCAGGCCGAGCTGACCTGTCTGCACCGAGTCCGGCTTGGCCGTGGGGCCCTGAAT - 7440
7441 - GCGGACACGTCAGTTTTGTGTTAAATAAAAGAAAGAAAGAGGTACAGGCTCAGCGTCCG - 7500
7501 - CTGCGAATGCCGCGCCCCCTCCCCGGGGGATTGCCCCACCCACTCGCGTGGCCTTCTGGG - 7560
7561 - AAATGTAGTCTTTTGAAGAAGCCTGGAATTCGCCAATAGGCGGACGAGAGTTTGGCGCA - 7620
7621 - TGCGCATAGGCGCACATGAAGCAAAAAGGGAAGTGGTGGCCGTCAACACCGGAACCCAGA - 7680
7681 - AAAGTCAAGTTTAGGGTACCGGGGAAATTCACGTCCACTGGAGGAAGAGACTTAAGGC - 7740
7741 - TACGCCCCACTCCCATATTTTGACCCGGAAGTTATTTATTTTAGCGTAGAAGACTACTTTT - 7800
7801 - CCCGACGCGCCCCAGGAAAGTGCCCTCGATCAGTTTCCTAAGGGCCCGAGTTAGACTTTT - 7860
7861 - TTTTCTCTTCCAGCTTTTGGGACTTGGGGGCCGGACAGGTCGTCTTTCTTGGGGTA - 7920
7921 - TCCGGGGTGCGGACAAGGTGGGAGAGCCCTACGGTATCCAAGCTT - 7965

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Fig. 24 (1/9)

1 - CAACATGCTTGGGACCAGAAGTGTTCCTCAATTTGGGATTTTCTCAAATTTTACCGGTTGA - 60
61 - GCTTCCCCAATCTGAAAATCTGAAATCCAACATGCACGGCTCTGAAGTCTTTCAGTGAGC - 120
121 - CTTTGGGGGAAATATTTAACATCCTAACAGCCCTAAACCAACGCTCAATTAGCACAAACAG - 180
181 - TTTACAACTCTCTCTACCCACAGCCTGATGCGAGGCTCTGGGACTAGACTATTTAGCCAA - 240
241 - CAGTCTCTTGCAAAATTAAGTACTTATAAGTAAATAGTAATTTCAACACCTCACTGCTAA - 300
301 - TGCTGTAAACAACTCTGCAGACCTAGGGAGCAAGTACGGTTTGCAGAGCACTGGGAAGGCT - 360
361 - CTGAAGTGACCTTTGAACTGGGCCTCAAAAAATTTTGGGTTTGGCAAAAGTCAAATCTCT - 420
421 - TAGGCTTCAAATTCAGGCACAAGGATTGTTGGGTTTGAATTCATTATCCAGAAGCAATG - 480
481 - GGGATACAGAATTGTGATCTCATGTGTAGGGAAGTGTGGGGTTTCTACTTTAAGCC - 540
541 - CAGTGAGACTTTGTAGAGTGTGGGGTAGAGAAAAGGCTCATGAATATGCCTGAAGCCTAA - 600
601 - CTCAGCACCTTTCTGAGGAAGTACTGCCAAAATGGTAATGGAGAGGGGAAAATATGACC - 660
661 - TACTTTTACAAGTTACCTTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTCTTCTTCTGG - 720
721 - GTGAAAGACCAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAGTTTGAATCCCTGT - 780
781 - TTTAACCCTCACTATCGATATGACCTTGGATAAGTTACCTAACCTTTCTCTTACTGTCC - 840
841 - TTTTCCGTAAAATGGGGATAACAGATAGTAGTTATTTCTATGAGTGGTTATGAGAACCAG - 900
901 - GCTATTAGATAGCGGGAAGCACACAGTAAGCGTTCAAGGAAGTCTATTGTTATTAATAA - 960
961 - GCCTCCTTTTGAAGAAGGACATTGAGGCCAGAGAGAGAACAAGCAAGTCCAGCCACACAG - 1020
1021 - CAAATCCGTGATGAAGTTGGGACTGGAGTATGGGTCTCCTGAGTCTCAGCCAGGACTCT - 1080
1081 - ATCCCTCTTCCCGAGTCTCGGAGTTCCCGGATGGAGTCACATTTGTTTACCGCCAGGGA - 1140
1141 - GGAAGGTTTGTGAGGAGCCTGCAGGAAACAACAGCCAGGCGCAAGGCTTTGGGAGTTGAA - 1200
1201 - GCATAGCTTCTGCGAGATAGAAACAAGGTTGACATGGGCACTCGTGCAGAATGACGGGCT - 1260
1261 - CCTTTTGGACTCCCAGGACTACAGTCCCTTATGCACCTTGGGATCTGCGGCTAGCCCTG - 1320
1321 - CGTAAAGAGGGACGCGTAGTCTTTTCCCTGCCCCGCCCTGCCGGGGCGCCCGCTCCGAG - 1380
1381 - GCCGCCCTCGCTTCGTCTTCCAGCAAGCTCCGCGCCGGCGCCGGCTATTGATTGGCTG - 1440
1441 - AGCGGGAGCAGGCGGCTGGCCGGCAGCAGTTACTCGGGGTTTCCGGTGCAGGGCCAGAG - 1500
1501 - GTGGGGAAGCCATCGGACGTCGGCGGTGAGGTACGTGCAGCGCGCGCGGTTGGGCGAGAC - 1560
1561 - TATTTGAGAGTGTGCGGGCCGGGATGTTCTCGGCCTGTGGGGAATCACGCCAACTCCCC - 1620
1621 - GCGTGGGCGGGGGGCTGTCTGGGGATATGCGCATGCGCGGGCGTGCCTCGCGGCTTGAGG - 1680
1681 - GCGCGCGGGGCGTGGGTGGCTGCGCGCGCGGGGGCGCACGTGGGGCCTGAGGGGCGGGG - 1740
1741 - GCGGTGCCGGGAGTCCCGCCACGTCACTCCGGCCCTGAGCCAATCCCGCGCCCGGCT - 1800
1801 - GCCGCGAGGGGGCGGTTGTGCCGGGAAGTGGCTCCAGGGAGAAGAGGCTCTTCCCTCA - 1860
1861 - CCCGCTGTGGGAGCTGCGCCCCGAAAGCCTGCCCGGCACGTGCGGCTCTCCTGACCCGC - 1920
1921 - CAAGACCAGAGAGCCGTTGGCGCCCTCCGCCGGGCTGCCGGTCCGTTTATTTTAAGAA - 1980
1981 - GCTTTGTGCGCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGAATTTCAAGTCTGGA - 2040

2041 - AAATAGCAACTGTGTTTGTCTTAAAGGATCTTCTCCTGACCCAGCATCGCTCATCAAA - 2100
M

2101 - TGAAGAACCAAGACAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAGCAGCCAG - 2160
- K N Q D K K N G A A K Q S N P K S S P G

2161 - GACAACCGGAAGCAGGACCCGAGGGAGCCAGGAGCGGCCAGCCAGGCGGCTCCTGCAG - 2220
- Q P E A G P E G A Q E R P S Q A A P A V

2221 - TAGAAGCAGAAGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGAGGGTGTGTGCCAGC - 2280
- E A E G P G S S Q A P R K P E G

2281 - TCTGCGTTGCCAGCGGGCAGGGGGAGGAGCTGTGGGGTGGGCTCGCTTCTGGACTTACA - 2340
2341 - GGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGTGGGGGCC - 2400
2401 - GCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTTAAGCACAGGAACAGA - 2460
2461 - GTTCTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520

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Applicant(s): Ann M. Lees et al.

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Fig. 24 (continued, 2/9)

2521 - AGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGTT - 2580
2581 - TGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTGTGGGGGGGAAGGAGAT - 2640
2641 - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT - 2700
2701 - AACAAATATGTTTCGGGTGGTAGTGAGAAATAGTTGTGTCAATTTACAAGTAAACAGACTT - 2760
2761 - AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTAAAAGATGTTTCGAATCTAAAT - 2820
2821 - TCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA - 2880
2881 - AAAAAAGTTAGGCAACATTTAACTCAAACCTGATGAGTTTGGCTGGGCCTGAAAAATCCCA - 2940

2941 - ACCAGTGGTATAATCGTCTTCTTTCTCACTCTACCCCTCATCCTCTCTGCTGTAGGGGC - 3000
- A

3001 - TCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCA - 3060
- Q A R T A Q S G A L R D V S E E L S R Q

3061 - ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGA - 3120
- L E D I L S T Y C V D N N Q G G P G E D

3121 - TGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGTGGC - 3180
- G A Q G E P A E P E D A E K S R T Y V A

3181 - AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGAAGGAACCTCCAAGGG - 3240
- R N G E P E P T P V V N G E K E P S K G

3241 - GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTGCGAGACCGAGACCATCGAAG - 3300
- D P N T E E I R Q S D E V G D R D H R R

3301 - GCCACAGGAGAAGAAAAAAGCCAAGGGTTTGGGTGAGCAGAGGGCGGCTCTTTGTGAAGC - 3360
- P Q E K K K A K G L G

3361 - TGGTGAGGAGAGGGAGTTTGGACTTGACGTTCTCTGGGCCAGTCTGTTCTGCCAGGATTC - 3420
3421 - AAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTCTAGTCTAATCAAAGCCAGGGATG - 3480
3481 - TGGGGGCCACGGCATAGAGAGATGCAGGAGTTACCAGCACAAAGCCTTCTGGGTTTTGGA - 3540
3541 - GCAACTGGAGCTTGGCATGGGACCTGTTCTCTCTTTGAGAAAATGGAGACGGGAGGCTAG - 3600
3601 - GGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGTGACCTTGGGTGTGTCCCTTCTCC - 3660
3661 - TCTCTGGGTCTTAGTTTATATTTCTCTTTACAGTAAGAAAATTAGACTAGGCCAGAGTTG - 3720
3721 - AAAACCCAAATATCTGCATAAGCTGGGCTTGGCCATGGGGCCACCTGAAGATGGAGGCTT - 3780
3781 - TACTGCTTCCCTGATTAGTTGCTCTCACTAGCCAACCTGAGAGCAGGCAAACTACAGGCT - 3840
3841 - GGGTGCACTCAGGCTTTTTTTTTTTTTTTTTTTTTTTTAAATAAAGAAAAGCCAGAAATCT - 3900
3901 - AGAGTTATGTGAGAACTCTAGATTTTTTTCATAGTTAGCAGCTAAAATGGTAAGAGCCAAA - 3960
3961 - CAAAACCCATCCGTGGGTTGGATTTGGCACACATGCCTGCGAATTGCAGTCTCCATGCTG - 4020
4021 - ATCTCTTGGGCCCTTCTGGGGAGGCAGAGGGAAGGCTCCCTGACTCAGTCACAGGCAATG - 4080
4081 - GGAATAGGCAGTGACAGTCATTTTACAGCAGGGTATGTATGTTTAAGAGTCTAGGCCGG - 4140
4141 - GGTGTGGTGGCTCACGCCTGTAATTGCAGCACTTTGGGAGGCCGAGGCGGTGGATCACC - 4200
4201 - TGAGGGTCAGGAGTTCGAGAACAGCCTGGCCAACATGATGAAATCCCGTCTCTACTAAAA - 4260
4261 - ATACAAAAATTAGCTGGACATGCTGGCACACGCCTGTAATCCCAGCTACTTGGGAGGCTG - 4320
4321 - AGGCAGGAGAATGGCTTGAACCCGGGAGGCAGAGTTGCAGTGAACCTGAGATTGTGCCAC - 4380
4381 - TACATCCAGCCTGGGTGACAAGAGTGAACCTCTGTCTCAAAAAAAAAAAAAAGAATCTA - 4440
4441 - GAATCTAAGTCGAGTGTCTATTATATCCATGTTTATTCCTATTCCTTTTCCCCTTATGT - 4500
4501 - ATCCTCTTACTTTAAAGAGGAACTTTAAAAAATCTTAGGGACGACTAGGCAGAGTGGCTC - 4560
4561 - ACACCTGTAACCTCCAGCACTTTGGGAGGCCAAGGCAGGCAGATTATGAGGTCAGGATTC - 4620
4621 - GAGACCAGCCTGGCCAACATGGTGAACCCCACTTCTACTAAAGATACAAAAAATCAGCC - 4680
4681 - GGGCGTGGTGGCACGTGCCTATAATCCCAGATACTCGGGAGGCTGAGGCAGGAGAATCAC - 4740
4741 - TTGAACCCGTGAGGCAAAGTTTTTCACTGAGCTGAGATCATGCCATTGCACTCCACCTGGG - 4800

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Fig. 24 (continued, 3/9)

4801 - TGACAGGGTGAGACTCCATCTCAAAAAAGAAAAAGGAAAAATCTTAACGTCACATACA - 4860
4861 - TGGAAAGATCATCTTTTACCCCCCACTGAGATGGAGTTTGGCTCTTGTCAC - 4920
4921 - CCAAGCTGGAGTGCAGTGGCGGATCTAGCTCCCTGCAAGCTCCGCCTCCCGGGTTCACA - 4980
4981 - CCATTCTCCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTGCTACCATGCCC - 5040
5041 - GGCTAATTTTTTTGTATTTTTTTAGTAGAGACGGGGTTTCATCTGTGTTAGCCAGGATG - 5100
5101 - GTTTTGTATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA - 5160
5161 - GCGTAAGCCACTGCACCCCGCCTTTTTTTTTTAATTAATTTTTTTAGACAGAGTC - 5220
5221 - TCGCTCTGTCCCAAGCTGGAGTGCAGTGGCGGATCTGGGCTCACTGCAACCTCCGCCTC - 5280
5281 - CTGGGTTACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTG - 5340
5341 - CTACCATGCCCCGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCACTGTGTT - 5400
5401 - AGCCAGGATGGTTTTGATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTCC - 5460
5461 - GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTAAGCCACTGTACCCTGCCTTTTTTT - 5520
5521 - TTTAATTAATTAATTTTTTTAGACAGAGTCTCGCTCTGTACCAAGCTGGAGTGCAGTGG - 5580
5581 - CGCGATTTGGGCTCACTGCAACCTCCGCTTCTGGGTTCAAGCGATTTTCTACCTCAGC - 5640
5641 - CTCCGGAGTAAGTGGGACTACAGGCGGTGCCACCACACCAAGCTAATTTTTTTGTGTAT - 5700
5701 - GTCTTTAGTAGAGATGGGGTTTACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA - 5760
5761 - TCCGCTGCCTCGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTTGCCTGGCC - 5820
5821 - GAAAGTATCTTCAATTTAAAGTTCACTGTTGGCTACTCTGTTGACAAGAGTTTAGTATT - 5880
5881 - TCTCAAGGAGGCTAAGATACCTATTCCTTTTGGACTCTACCTCTATCAGGAGGGTGGGC - 5940
5941 - CTTCTTGCATTGAAACAGTATGAAAACAGTAGCCCTGAATTCATAAGTGGGACACCTTT - 6000
6001 - CTTCTATTGGTAGAGCAGGCAGTTTTTTTTCTCCTGCCAATGGTGCCTACTAAGGAGATTT - 6060
6061 - CACTAGGGTACAGTCGTTTCAATTTGATAAGCATTTGTTGAGCATATCCTCTGTGATGGTAC - 6120
6121 - TATGGACAGTACTGGGGCTATAGTGAGGGCAGGATTGAGTTGGTCCTTATGGCAAGGAAG - 6180
6181 - GCAGCTAATCAACAAGCAAAATATAAAGTATGATGGGGAGGGCTGTCTTCAGCACTCATG - 6240
6241 - AGTGTGAGCCCAGGCTGGAGGGGACACCTGGAGAAGAGGGTGCATGTCTTTGCTCCTGT - 6300

6301 - GCTTTTCAGGGAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCCAG - 6360
- K E I T L L M Q T L N T L S T P E

6361 - AGGAGAAGCTGGCTGCTCTGTGCAAGAAGTATGCTGAAGTGGTCAGTTCCCCCTCCGCG - 6420
- E K L A A L C K K Y A E L

6421 - GGCACCTTCCCTGCGTTGGGAAAATCAGCATGCCACCTGGTGTAAAGTTGGGGGTGCAGA - 6480
6481 - GTCAAGTAGGTGGCTTAATTCCTGTTTCACTTTTCTCTGAAGTATCTGTTAAATGGGGAA - 6540
6541 - TCACTTCCAGCCAGCCTCTTCAGGGCTGTGCAGCAAGAGGAGAACTGCATATTCCTTGA - 6600
6601 - AAGAAATTTCTCAAAGAATGATTCCAAGGTGGTAGAGCCCTTGTCTCGCCTGAGTCCA - 6660
6661 - AGACACCTTGTGATCTTGATGCTTCTTCCCTCAAATACAGATGCATAGAGCCATTATCACA - 6720
6721 - GTTAATAAACTAACACTAGTCACTTGATACTTTTCCCTTTTACTCCAGAGCAGTCTTCT - 6780
6781 - TGTAAGTGCCTCCTCATATTCCTCATGACATTGACTTTTAAAGAACTAGACTAGCTGT - 6840
6841 - CTTGTAGGATGCCCCCTTCTAGCTTTGTCTATCTCTGTGGTATCATTTTACTTCTTTACCT - 6900
6901 - CCTGGTACATGTAAGTGAAGTAGAAGTTAGCTCTAAAGCTTGATCCAATTCAGCTTCAAC - 6960
6961 - TTTTGGACAAGAATCTTCATAAGTACTTCATGTTCCATCACAATAAATGCAAAGCATGC - 7020
7021 - TCTTCCCACTTTGTTGTAACATTGTTCAAGTGGGTTGGGGGTGGGGCAGCCAGATTCTTCC - 7080
7081 - ATCATCAGGTCCCTTGTGCAAAATTTGAAGTATGATGTTTATTTATTTATTTATTTTATTT - 7140
7141 - GTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT - 7200
7201 - GGGGTCTTGCTCTGTGCGCCAGGCTGGGGTGCAGTGGCAGCATCTCGGCTCGTCAAGC - 7260
7261 - TCCGCTTCTGGGTTTATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGTCTACAG - 7320
7321 - GCGCCCGCCACCATGCTAGGCTATTTTTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGGT - 7380
7381 - TTCACCGTGTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCCGCCTCGGCC - 7440
7441 - TCCCAAAGTGCTGGGATTACAGGCTTGAGCCACCACGCTGGCCTATTTATTTATTTATT - 7500
7501 - CAGAGTCAGAGTCTCGCTCTGTCAAGGCTGGAGTGCAGTGGCGGATCTCGGCTCATT - 7560
7561 - GCAACCTCCACCTCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA - 7620
7621 - TTACAGGTGCATGTCACCATGCCTGGCTAAATTTTGTATGTTTTAGTAGAGACAGAGTTT - 7680

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Ant(s): Ann M. Lees et al.

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Fig. 24 (continued, 4/2)

7681 - CAGTATGTTGGCCAGGATGGTCTTGATCTCTTGGCCTCGTGATCCGCCCCGTCTCAGCCTC - 7740
7741 - CCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCTGGCCTCTAAGTATTTATTTTAA - 7800
7801 - AATTAATTCATTCCACACACATTTATTAATATTTTCTGTAAAGGAACCTTACTCATCTTT - 7860
7861 - AAAATGGGGAATGTACATACCTGCCTAATGACATTCTTGTAAAGGATTAATAAAAAGGTATA - 7920
7921 - AGGAAGATAAGCACCCCTTTTGGAGTGATCCAGCCAGGGGAAAATTGCTGATGCAAGAGAG - 7980
7981 - GAAATGAGTTGCTAGAGTGGTGTGTGTGAGTAGAGGAGGGGAGCTGAGGCCTGCCCCAAGAA - 8040
8041 - GGGGGCTTGGCTGTGGTAACCACATGGCTAGGTCTGTGTGACTGGAGGAGAGGACGGGGC - 8100
8101 - AGGTGGACTGGTAGATGTGCAGCTTGTGCCCTGATTCTCTAGTTTCTTCTGTGTTTTGA - 8160
8161 - GATTTGATGAGAACGATGAAATAGTTGTCTGGAAGGAGAGGAGTGTGAATAGCATATGCA - 8220
8221 - TTGTATTGGGATTGCTGGTCTTCTGAAATTGGTGGCCATGAATTTAAAGTGAGACTCTT - 8280
8281 - CAAGTAGGGTTGTTATAGTACTGGTGTAAAGCAGGAAGGTGCTTTACTAGGGTTGCAGTA - 8340
8341 - CTACTGGGGAAGGGCCAAGAGAGTTGAGGGTGTAAAGAAATCCAAGCCAGGTAATGTAGTT - 8400
8401 - ATTTTAAAGGAGAGTGGAAGGATGGTTGAGTCAATGGATTGGAGGTCTATAGGGTAAGA - 8460
8461 - GACTTTCTGAGGATCACAGATACTGATTGGAATGAGCTAAAAAGATAGGTGATGGTAGTC - 8520
8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTCTGGTAGTGACAAATCTAG - 8580
8581 - ATCTGCGCTGTCCAAGATAAATTCGTCTCTAGCTAATTGACATGTGGCCAGTTTGAATTT - 8640
8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTTTGAAGACTTAAGCAAAAACAAAGAA - 8700
8701 - TATAAACATCTTTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760
8761 - ATGTCCTGCTTCCAGGTTCAAACGATTCTCCTGCCTCACAGCCTCCTGGAGTAACTGAGA - 8820
8821 - TTACAGGCGCATGCCACCAAACTGGCTACTTTTTTGTATTTTTTTTTTAGTAGAAACGGT - 8880
8881 - TTCACCATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCTGCCTGCCTCAG - 8940
8941 - CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACTCCCGGCCTCACTTTTTTACAT - 9000
9001 - TGATTCCTGTGTGAATTTGTAATGTTTTTGGATATTAGGTAAATACATATATTACTAAAA - 9060
9061 - TTAATTTACCTGTTTTTTACTTTTTTAGTGCGGCCAGTAGAATATTTTAAATTACTTAT - 9120
9121 - GTGGTTTGCATTATATTTCTGTTGTACAGGCCTGGATAGGGTCATGGGAGGGGAAGT - 9180
9181 - CTGGGGAAAGGAGTGGGTTTGTGGAAGAGGTGATGGACTGTGAGGCCAGGGAGTTAGAAG - 9240
9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTGTTGGGGAGAGCG - 9300
9301 - CTGATGAACGCAGCGCTAACGTTTTGAAGGAATGCGAGGGAGCGATGGGGGTCTGTCTGT - 9360
9361 - TAATAGGCACAAGGTACGGTAGCAGGTGGTCTCATCCTCGGGCATGAGTGTCCAGCAAGT - 9420
9421 - TGGGGAAATGCAACAGCTTGAAGTGGCTCTAGTGGCCCAGAGTCAGAGCTGGAATAGGAA - 9480
9481 - TTGGCATCTGCTGGCTGTGTGGCCCCCTGCTTGCCCTAGTGAGTTACCATTTCTGTCCC - 9540
9541 - TACGGTGGAGCCTTTGGGGTTATTGTGAGTTTCATGGGAGGAGCGTGTAAAGCACCGGCACA - 9600
9601 - GCATCAGCCCATGAGAGTGCTCCTGGCCTGAGAGGGTAAGGGTCAGGGCAGCTCAGGAGA - 9660
9661 - CCCTAGACCTGCATAGTGATCCCCCACCAGGAAGGCCCCACAAGATGCTCACCTGCCCT - 9720

9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTA - 9780
- L E E H R N S Q K Q M K L L

9781 - CAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCACCTGCGCGGTGAGCACAGCAAG - 9840
- Q K K Q S Q L V Q E K D H L R G E H S K

9841 - GCCGTCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900
- A V L A R S K L E S L C R E L Q R H N R

9901 - TCCCTCAAGGTAGGCCTGGGCCCCCTGGAACAGGTGACTCTGGTTTCTTTGACTTCCACT - 9960
- S L K

9961 - TAATGTTTCTTTTCATGGGCTTTCTCTTAAAAAGTAGTGCAGGCTAGGGCCAGGCGCAGT - 10020
10021 - GGCACACATAAGTGATTAAAAATCTTCTGGCCACTAAAAAACAGAAATTAATTTTAGTAA - 10080
10081 - TATACTTAACCCAATATCCAAAACATTACAATTTCAACATGAAATCAGTGTAAGGAAAGCA - 10140
10141 - AGGCTGGGTGTGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGATGG - 10200
10201 - ATCACTTGAGGCCAGGAGTTTGAACCAACCTGGTCAACGCAGTGAAACCCCATCTACT - 10260
10261 - AAAATACAAAATTAGCCGAGTGTGCTGGCAAATGCCTATAATCCAGCTACTCAGGTG - 10320

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Fig. 24 (continued, 5/9)

10321 - GCTCAGGCATGAGAATTGCTTGCACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380
10381 - TCACTGCATTACAGCCTGGGCAACAGAGTGAGACTCAGTGTCCAAAAAAAAAAAAAAGTA - 10440
10441 - GTGCAGGCTTGTGGCATAGAAATACACTTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500
10501 - GCTTGTAAATCATTGACATGTATTAGATAAGGTGAAGGATAAAGTACTAAGAGAATCCAT - 10560
10561 - AATGCACTGGCGTTAGTATTTCTCAATGAAATGACAGTCCCTTGGTAAGCGGAGGCCTGG - 10620
10621 - CTCTGACAAGCAGCTCTTGTCCAGACGTTGGTCAGTCAGGAACCTGGGTCCCTTCCCATG - 10680
10681 - TTCTGCTGCTTCTATGGTGAGGTCAGTCTGTGGTTACACCAAGTTTAAATACAGCCTTTT - 10740
10741 - AACTTTCTTTTTTATATGTAAATCTTACATGTAGTTTTTGTAGTAAATGAAATTATTATACAT - 10800
10801 - GTACCATTTTCATATCCTGTGCCTTTTTTCACTTTACATAACATTTTTCCCTATCAGTAT - 10860
10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATATCAGTGCCCTAGTTAAAGCATTT - 10920
10921 - TGGGGGTTGTTTACAATTTTTCATTATTACATATAGAAGTATAGTGAATGAAATTTCTGTTAT - 10980
10981 - ATTTATCACTGGTCAGTTATATAGAAGTATCTGTAGGATAAGTCATGGAATGAAATGG - 11040
11041 - CTAGGTCACAGTATATGCAGATTTTTTCATTTTAATAGATTTTGTGCTGGATTGCCTCCAGT - 11100
11101 - GAGGGGGCAGTGTGCCTTCCCCATCAAAGTGTTGAGTGCCTAATTCTGCACAACCTTTGC - 11160
11161 - AAACCTGGGTGTTACTAAATTTTAAACAGCTTGGTCTCTGGGGGTACAGAGGGGACAAAT - 11220
11221 - GCACATTAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTTCAGAATGG - 11280
11281 - CACTTAGCACTTACATGTGTGCATGTGTGCCTGCATTTTTTCTTCTTTTTTTTTTTTG - 11340
11341 - GGGACGGAGTCTTGCTCTGTGGCCCATCGCCAGGCTGGAGTGCAGTGGCGCGATCATAG - 11400
11401 - CTCACCACAACCTCCGCTCCAGGTTCAAATGACTCCTCTGCCTCAGCCTCCCAAGCAG - 11460
11461 - CTGGGACCACAGGTGCACACCATCACGCCGGCTAATTTTTGTATTTTAGTAGAAACGGGG - 11520
11521 - TTTCAACCATATTGGCCAGGCTGGTCTCAAACCTCTGACCTCGTGATCCGCCACCTCAGC - 11580
11581 - CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCTGCCATGTGCCTGCATTTTTT - 11640
11641 - CTAGGGGGAGAATCTCACTTGATGTACCTGATATACAGAGGGGGCCATTGGAACCCGCA - 11700
11701 - TTGCACAACATCCTGGAGTCTGGCTACTCCACGCTTTGGGAGCAGGGAGGGCTGTTGGCA - 11760
11761 - GAGACCATCTGTGGACTAGCTGGGGGACCCTTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820

11821 - GGCTGACTTCTTTGCCAGGAAGAAGGTGTGCAGCGGGCCCGGAGGAGGAGAGAAGCG - 11880
- E E G V Q R A R E E E E K R

11881 - CAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTAGCTGCAGATGGAACA - 11940
- K E V T S H F Q V T L N D I Q L Q M E Q

11941 - GCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCTGAGAGGCTCAA - 12000
- H N E R N S K L R Q E N M E L A E R L K

12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAGGGTATCACGGACAGCAGTCAT - 12060
- K L I E Q Y E L R E E

12061 - GGCCAGAAATTGTGAGGTTTTGAGTGTGTGCTAGGCACTGGGACAGTACCTTTTCAGGC - 12120
12121 - TTCATCCCATTCTCCCTTTCTTCTCCTCCTCCTCCTTGGGAGGAGAGTAATGTTATTCC - 12180
12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGACTCACTTACAGCCACACAGCCCCAGGTCC - 12240
12241 - ACAGTGCCTTGTCCCAATGACTGGGCCAGGCATCTTTTGAATTAGAACTATCCACATT - 12300
12301 - TTAGAATGGAGGTACATGTATGGACTGTGTGTTATATAGCACCCTCAGCAGGGCCTTGGG - 12360
12361 - GAAGCCAGACACATTAATGTATTTATGCACTAGAACTTCAAATACTCACCTACATTATG - 12420
12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTTCCATTTTCAGAA - 12480
12481 - CTTTGTAGAATTTGGAATTGCAGGGGAGGGGTGTACCTGTGATCAGTGATGGACTCCAGA - 12540
12541 - GACTGTGTCCACTGATTCTTGTGCTGCTCCTGCCACTCAAAGGCAGAAATTTATCAGGCTG - 12600
12601 - GGCCTGGTGGCTCATGCCTGTAATCCCAACACTTTGGGAGGGCCAAAGCGGGCGGATCACC - 12660
12661 - TGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTCTACTAAAAA - 12720
12721 - TACAAAAAATTAGCCAGGTGTGGTGGTGCACGGCTGTAGTCCCAGCTACTCAGGAGGCTG - 12780
12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAATGAGCCAAGATTGTGCTAC - 12840
12841 - TGCACTCTAGCCTGGGTGATATACCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGC - 12900
12901 - AGGATGTCACTCCCTTTGTCACTGCGTTGGCTGCCACCCAGGCACTTGAATCTTTGGAT - 12960

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Participant(s): Ann M. Lees et al.

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Fig. 24 (continued; 6/9)

12961 - CTTCCCTGCCAGTCACCTGGCTGTTCTGGGCGCGTTCTCATCATGAGAAGGGAGACCTGC - 13020
13021 - AGCCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTTCTAGCCCCCTGG - 13080
13081 - GGTGTGGCAGTGGGTGAGACCGGGAAGATCTGCCCTCTTAGGTTTCATAGGCCAAAGTGAT - 13140
13141 - GATCGTGTGTGCAGGACCTAGAGGGCGCTCCCCGACCCACCCCTTTCTTGGCCATACTT - 13200
13201 - CATCCTCTGGGAACAAAGCTGCTTGTGTTGGTTTGAGGGGAGTTGGTTTGGTTCTTATCCC - 13260
13261 - TCAGCGCTGAGACATAGAGGCTTCTGGGCCACTACAGTGAGACACGAACCTTCAAGAATC - 13320
13321 - TGAATACCCCCGTTTTCTCTCCCCGCCAAGGCAAAAAAGGACTTAGTACTACCTGTGGAG - 13380
13381 - AAGGAGGTGCAGGACTACCAGGCCCTGCTGCTTTGCATTTACAGCCCTCCCCAGACAGAC - 13440
13441 - ACAGGCACCCCTCATCATACCCAACTGGACTTACCTGCTAGGCACCTTCCCTTCCCCATC - 13500
13501 - CAAAAAATGGAGTTATTTTCCCTTATTTACAGCAAGTCCAGTTGATTTTACCTTTGAAGT - 13560
13561 - AGCACCTGAGTCCTTACCTTCTCTCCATCCCTTCTCTCTCACCTGACACAGGTCTGCAG - 13620
13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCTTGGGGATGCACATGTCTAGTCTTTGCCTA - 13680
13681 - GATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTTATGTTCTTAGAGGCATTGTTTTTG - 13740
13741 - CCCATTCTTCCCATTTACAAGAGAATCAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800
13801 - GGTGATCAATCCTGGGGTCAGAGATTTGAGTGTGTTTATTGCTTGCCTTCTTGGGAGCAG - 13860
13861 - ATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTCACTGGGAGAGAAACGACGTGA - 13920
13921 - GGTGGAAGCTGACCTTCCAGAGACTTGGGGCCCATGTTGTGTGGTACACATGGGAGTC - 13980
13981 - CATCATATCAGATTGAGATGGGGGGCTGGGCAAAGTGCCCTGGTCTGTGGCTGTGGGGCT - 14040

14041 - ACCCTGAGAAAGGGAGCGCCTGACAAGCCGACTGCTCCCACCATCTTTGTTGCAGCATAT - 14100
- H I

14101 - CGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCA - 14160
- D K V F K H K D L Q Q Q L V D A K L Q Q

14161 - GGCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTTGTGAG - 14220
- A Q E M L K E A E E R H Q R E K D F

14221 - GCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGGAGACAGGCTGGGCTCTGGCTCAGC - 14280
14281 - TCATAGCCGGGTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCTTTGAGTACCA - 14340
14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGTGTCTGTGGCTAAAAACCAACATAGCCC - 14400

14401 - CTGGGGGCTTCTGACAGGATCTGGGGTCTGTCTTGGAAATAGCTCCTGAAAGAGGCAGT - 14460
- L L K E A V

14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520
- E S Q R M C E L M K Q Q E T H L K Q Q

14521 - GAGAGCATATAACCTGACCCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCATCCTGGGGG - 14580
14581 - TAGTGAAATGGGACCCTCATTCTAGGACTGGCTGTGTCTGGCTGCTATGACGCCTTGGT - 14640
14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGA - 14700
14701 - GGTAGGAACAGAAGAGTTTGAATCAACATAAAGGCAAAATAAAGTCACCCTAAGTCT - 14760
14761 - CCTACTTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGT - 14820
14821 - TTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAG - 14880
14881 - TGTGTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCC - 14940

14941 - ACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCAGAACACACTTTCCAAAAGCAG - 15000
- L A L Y T E K F E E F Q N T L S K S S

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Fig. 24 (continued, 7/9)

15001 - CGAGGTATTACACATTCAAGCAGGAGATGGAAAAGGTAACGTGGTCCAGGCCAGGCA - 15060
- E V F T T F K Q E M E K

15061 - TGGCTGCTGGGGCATAAGCTGCTTCATTCAAATTTGTTGGGCCTGCCTTCAGGAAGCTCC - 15120
15121 - CATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTACAGCCTTTCCCCTCTTGAG - 15180
15181 - GCAGTATCAGTGGTATGTATACACTCCAGGTTGTCCCAGGGAATGGGGCAGTCTTTTCTG - 15240
15241 - TTTGTTTGGTTTTTTTTGGGGGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG - 15300
15301 - TGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCATTGCAGCC - 15360
15361 - TTTGCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGACTAGCTGGAATTACAG - 15420
15421 - GCGCGTGCCACCATGCCTGGCTAATTTTTTCTTTCTTTTTTTTTTGTATTTTTTAGTAGAG - 15480
15481 - ACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGTGATCTGCCC - 15540
15541 - GCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGGCCCCCTTACC - 15600
15601 - ATTCCTTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGAGGTGGCACAGAGGGC - 15660
15661 - ATTGACTGCATCCTGTAATGCCTTGGCGCTTGGGATCAATCATTCCCCACCTTGGAGACA - 15720
15721 - CAGGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGAGGCCAGCTCTGACCATTTCCT - 15780

15781 - TCTGTCTGTACATAACCTAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACC - 15840
- M T K K I K K L E K E T T

15841 - ATGTACCGGTCCCAGTGGGAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGGTGG - 15901
- M Y R S R W E S S N K A L L E M A E E

15902 - GCTGTCTGTGATCTGCAGCCAGGGTGGGGGTGTGCACCTAGCGCATATCAGGCCCTTTCC - 15961
15962 - TGTATGTTCTACCCATCAGTGACACAGCTAGCATGAGGTAGAGGTGAGATTTGCACACAA - 16021
16022 - TGTCCAAGTCCAAAGTTAATGCTGTTCTCTCCCCATGGGAGGTGGTGAGCCAGTGGTAG - 16081
16082 - GTCTCCAGTGGGAGTGAAGGGAGCAAATGGAAGAAAGGAATAAAAGAGCAGAAAAAACG - 16141
16142 - GGTGCCAGTGATGTGCTGGTTTACATGTAAAGCAGCCCAGGTAGTTTGTGATTTACAG - 16201
16202 - CTTGTAATGTAGAAGAAAGGAACCTAACGATGGAGCAGCAACTGCAAGCCAGACCTTGCTG - 16261
16262 - AAAGTTTTTGGGTTTTTTTTTGTCTTTTTTGTCTGCTGAATGTTTTTAGGTACGTTGTTTAT - 16321
16322 - TGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAGATGAGACAGG - 16381
16382 - CTCAAAAGTCAAGTCCTTTGCCAAGGTCACGTGGTAGATAAATGGAGGAATACGTTATCT - 16441
16442 - CCAAGCCGTGCCCTTTTCTGCACCATGCTGCCCCACCTGACAGCCTAGTCATGGCTTCA - 16501
16502 - ACTAGGACTGTTTCTTAAAGGGGGCCAGCTTTGACTCGGTCTGCTCTCAGCCTTGTTAA - 16561
16562 - AGTGTTTGGCCCAAGTGGTGTAGTAAAGTGGGAGGTTGATGGGGCAGGCACTGAAGGT - 16621

16622 - CTCATTTCTTTCCCTAGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAA - 16681
- K T V R D K E L E G L Q V K I

16682 - TCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACAGAGCGCAATGACCTGAACAAGA - 16741
- Q R L E K L C R A L Q T E R N D L N K R

16742 - GGTACAGGACCTGAGTGTGGTGGCCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGA - 16801
- V Q D L S A G G Q G S L T D S G P E R R

16802 - GGCCAGAGGGGCTGGGGCTCAAGCACCCAGCTCCCCAGGGTCACAGAAGCGCCTTGCT - 16861
- P E G P G A Q A P S S P R V T E A P C Y

16862 - ACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACTGGGCCTCAAGAGCCCACCTCCG - 16921
- P G A P S T E A S G Q T G P Q E P T S A

16922 - CCAGGGCCTAGAGAGCCTGGTGTGGGTGCTGCTGGGAAGGGAGCGGCAGCCAGCCAGG - 16981
- R A *

LEVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING THEROSCLEROSIS

Fig. 24 (continued, 8/9)

16982 - CCTGGCCCATAAAGGCTCCCATGCTGAGCAGCCATTGCTGAAGCCAGGATGTTCTGAC - 17041
17042 - CTGGCTGGCATCTGGCACTTGCAATTTTGGATTTTGTGGGTGAGTTTACGTACATAGGG - 17101
17102 - CATTTTGC AAGGCTTGCAAATGCATTTATACCTGTAAGTGTACAGTGGGCTTGCAATTGG - 17161
17162 - GGATGGGGGTGTGTACAGATGAAGTCAGTGGCTTGTCTGTGAGCTGAAGAGTCTTGAGAG - 17221
17222 - GGGCTGTCATCTGTAGCTGCCATCACAGTGAGTTGGCAGAAGTGAAGTCTGAGCATTCTCT - 17281
17282 - GTCTGATTTGAGGCTCAGACCCCTCCCTGCCCTTCAGAGCTCAAGACAAGTAATACACCC - 17341
17342 - AGGTCTTGACTGCATTTGTCTTGTGAGCAGGGCTTGCTTGGTCAGCTCAGGCCCTCCTAG - 17401
17402 - CTGCTCTGGAGGCTCCTTTGATTCTCTAGACCTGGAAAAGGTGTCCCTAGGCAGAGCCCT - 17461
17462 - GGCAGGGCGCTCAGAGCTGGGGATTTGCTGCCTGGAAACAAGGGACCTGGAGAATGTTTTT - 17521
17522 - GCGTGGGATGATGTGCTGGTCAGGAGCCCTTGGGCATCGCTTCCCCTGCCCTTTGGTAG - 17581
17582 - TGCCAGGACCAGGCCAATGATGCTTCTCAGTAGCCTTATCATTACAGGTGCCTCTCTAG - 17641
17642 - CCTGCACAAATGATTGACAAGAGATACCCCAAGGAATATTTCTGAAGGTGTTTTTCTCT - 17701
17702 - TTATTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGACATGACAGTGTT - 17761
17762 - TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGTGCCTGGGTGCCTGGCC - 17821
17822 - TCCAGTGTCCCACCTCCTTACCACCCCACTTGGCTCCTTTGCCATCTTGATGCTGAGGT - 17881
17882 - TTCCTGTTTGGTGAGATCAGGTTGTTTGTGGTAAAAGAAAGGAAAGGGCTTCTGATGGCT - 17941
17942 - TTGCCACAAGCTTACCTGTGGGTTTTCAGTCTGAGAGGCCACCACAGTTCCCATCAGCA - 18001
18002 - CTGTCTCCATGCAGCAGTTGCTGGGTCCCATGTCCAGCTGCCTCTTTGGCTTCATGGGTT - 18061
18062 - TTTCTGCTTCTGCCCCACCCCAACATGTGCAATCCTCAAGATTTGTCCTGATTCTATT - 18121
18122 - TCCTGGCACCTCCCTGCCTGTCTTGGGGATTCTACTTCTTCTGCTGTGGGAGCCCATAG - 18181
18182 - CTGTTGTCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA - 18241
18242 - AATGGCTGCAGACAGTTGTTTCTGTGTCTGTTCTACCCCCACTCCAGTACATAACTACT - 18301
18302 - ATGTACTGTGTAGAGCCATTCTATATGCTGAATGTTCTGCTGTTGCAAAGTGGCAGGGT - 18361
18362 - ATTAGCCAGTGTTTGTGCCAAGCAGTTTTCTGGGACAACAGAATGACTCAGACCAAGATG - 18421
18422 - GATAGGATGGTTAGGGCTTTGCTTCTTGCTGTTTTTCTTTGAAGCTAGTTTCATTGTCCTG - 18481
18482 - CAGGTCCTTTCATCTCCATACCTAGCCCACTTTTAGCCCTTACCTTAAATCTCTCAG - 18541
18542 - ATAAGTTGGTTACAAAGGAATGTTAAGTACTGAATCATGTGTGACTGAGACCAGAGATGG - 18601
18602 - CAAATGAATGGCACCACTTTCTCCTTCTCCTGCCCCAGGGCAGGTACCACTGATCTGCA - 18661
18662 - TCAGAGTTGCCTGCTATTCTCTGGTGTATCCTTCACATCTAGGTGCCCTCAAGCAGCTGT - 18721
18722 - GTGAGTGTGAGATCTCTGCCATCTCTGGCTGAGATACTGCTGTCCTGTGAAGTGTTC - 18781
18782 - CATGACCTTTTTCTTCCCCTTTGAATCCCTCTGTCTGGAGTAGTCCTTGCCCTCTTCTGCTG - 18841
18842 - TCCAGTAGGGCCTTTTCCCTACCCAGCCCCCTGTGCCAGGCTAAGCTGGTACAAGAGCTG - 18901
18902 - CCAACCTCACAGAGTGTTTGTCTAGGCGAGAGAGGTGCAGGGAAGAGGCAGAGGTATGCAC - 18961
18962 - CTTCCCCCTTGAAGAGAGGGGAAAGGCCTACAGTGGCCACATAATTGCCTGACTCACAC - 19021
19022 - TTCAGCTACCTCTTAATGCCTGTGGAGGGACTGGAGCTGCTGGATCCCAGTGTGGTGGTG - 19081
19082 - TAGGAGGCCACAGTGAGCAGGTGGCCCCAGCTGGGTTTCCCAGGTGAGGAATGTGGGCC - 19141
19142 - CAGGCAAGGTGCAGCCTTTGCTCACAGCTCCATCCATGTCTAGACCTTCAGGCCAGTCTG - 19201
19202 - CAGATGAGGTTCCCTACCTTTTTCTTCTCTTTCATTGACCAAATCAACCAATCACTACAGC - 19261
19262 - TGCTCTGCTTCTGCTTTCCAAAGTAGCCACAGGTCTGGGCCAGATGACGGGGAGGTGCC - 19321
19322 - ATCCATGAGTGAAGGCCAGTGCTTCTCCACCTGGGTGGGTCCCACACTTGTGACCTCAG - 19381
19382 - TTTTAGGACCAAGATCTGTGTGGTTTCTTAGATTGCTAGCTTTTCTCAGGGGACCAC - 19441
19442 - AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTTAGGGCCTTGT - 19501
19502 - CCAGCTGAGAGCTTCATGTCCACCAGATTCTGAGAGGTGTGAGCAGCACTTTTTTTTTTTT - 19561
19562 - ATTTGTTGTTTGTGTTTTCCATGAGGTTATCGGACCATGGGCTGAGCTCAGGCACCTTCTGT - 19621
19622 - AGGAGACTGTTATTTCTGTAAAGATGGTTATTTAACCCTTCTCACCCCATCACGGTGGCC - 19681
19682 - CTGAGGGCTGACCCGAGGCCAGTGGAGCTGCCTGGTGTCCACGGGGGAGGGCCAAGGCC - 19741
19742 - TGCTGAGCTGATTCTCCAGCTGCTGCCCCAGCCTTCCGCCTTGACAGCACAGAGGTGG - 19801
19802 - TCACCCACAGGGACAGCCAGGCACCTGCTCCTCTTGCCCTTCTGAGGGGAAGGGAGCTGCC - 19861
19862 - TTCTGTCCCTGTAAGTCTTTCCTTATGGCCCAGCCCGGCCACTCAGACTTGTGTTGAAGC - 19921
19922 - TGCAGTGGCAGCTTTTTTGTCTCCTTTGGGTATTCAACAGCCAGGGACTTGATTTTGA - 19981
19982 - TGTATTTTAAACCACATTAATAAAGAGTCTGTTGCCTTACTTGTGTTCTCTCCTGACCTG - 20041
20042 - TGTATTCCTTTGTTTCTGGATCTGATCCATTACGCCCCCTCCATCATCACTGACTGTGTT - 20101
20102 - AGGCTGCTGCAGAGCGCCCATGGTGGTTCCTGATTACTTACATATTCACAGTGTCTT - 20161
20162 - TGAGCAGTGCACAGCCACAGCTCAGAGTCTGGCATATTACTTGAAGTGCCTGAGTGGAGCC - 20221
20222 - CTTGGCAAAGTTGGCAAGACCCCTTGCCCTCAGAGAGGATCACACACACACAAAAAGTTTT - 20281

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS
AND THEIR USE IN DIAGNOSING AND TREATING
ATHEROSCLEROSIS

Fig. 24 (continued, 2/9)

20282 - CCCTGACCTGGGGGCTCACAGGCTAGTGAAGGGAAAAGGTACTTTTAGCTATAGACAGGT - 20341
20342 - CAATGGTGCTGAGAGCAGAGAGGAGGCCCTGCCCCCTTCAGCAAGGTGAGGGGGTGATA - 20401
20402 - CCTGGAATGGCCTTCTGAACCACAGGGCAGGTAGAAGATGAACGTCATTTAGTGATTAAA - 20461
20462 - TGGTACAGCTGGGAAGCAGGTCCATGGGACTGGGAGAGGGGGTGAGGCTGGGCCCAGAGT - 20521
20522 - CTGGGTACCAGGTTAAGGAATGTGGGCTAGATCCAGAGGGCAGGGGGGGCAACTGAAGGT - 20581
20582 - GTTCAATAGGAAATTGATAGGCTCCAGCAGTAAGGCAAAAGGCATGGAGCCAGGCATAG - 20641
20642 - GCCATTTGAGGCCAGGTTAAGAGGGGTGGACACTCATCACTGCTATTTGGGTCTGAGCT - 20701
20702 - GTGGGTAGGCTCCTATAGCCCTGGCCCTGCCCAAGGGAATTCACAGGGGCCTCTAATTGTA - 20761
20762 - TGCATTCCTTAAGGAGAGCACATTCTCTGTTCACTTTTTACACCCCCCATTTACCCACCT - 20821
20822 - CAAGCATGGGACTCCTATATGGGAGACATGCTGCTGGTGGCCTCACCCAGCACCTGTTC - 20881
20882 - TCTCTGGGTCTGGGTTGGTCAGGCACAAAGGATGATATGTGCTGAATGCCCAGGAAATG - 20941
20942 - GCAGAGACAACCCACCTGCCCTTCCCTCCAGGCCTCCACAAATAGATGTGCCACAATGA - 21001
21002 - CTGTGACAGTCCCAGCAGAGCCTCTGACCTTCTAGCTGGGTCTGATACATGTTTCCA - 21061
21062 - TGCTGGCCATGTTATTTCTAGTCGCAGATCCTCTGGAGGGTGTGGGGGGGTGCCGCCCT - 21121
21122 - AACTCTTGGAGATTCCAAGCAAAGCAGCTCTGAGAATAATGAGGTTTCTGACCCCCAGT - 21181
21182 - GAAGCAGCTGAGGATGGGAACCACAGGGGTGCTCCCTCTGTGTCAGCAGCATTACCACTGTC - 21241
21242 - TACTCTAGCAGCTCCGGTGGGGAAGGAGAGGGATTCTGTGTCCCCAGTCTGGGCCCT - 21301
21302 - GGTTATTGAAAAAGTTCGGAATTACTCTTTACCCTTGTGGAGTGTTCTGAGTGTTGGAAG - 21361
21362 - TACCCAGGAAGAAGCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCCATGGCTCCCCACATC - 21421
21422 - AGCCAAGAGGCCCAACCCAGGAAGCCACTCCTGCCCCGGGGATGGGGAAGGTGGGCTGGG - 21481
21482 - TGGCTGTGTGCACTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCTGGCCAAACA - 21541
21542 - TGAGCCTCTCTCCTGTGTATCAGATGCTGTTCTGGGGACCTGCGCCAGGAGCCTCTGCC - 21601
21602 - AGGGCTTTAAATAGCTGCCCCCATTGATCTGGCTGCAGGCAGCAGCAGTCACACTGGGTC - 21661
21662 - AGCCTCCATCAGGTGCTCAGGTTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721
21722 - GGTCTACCTTATGACCTGGTGCTCCCCACACCTGTCTCCTAGGCCTGGGGGGTGGGGAGG - 21781
21782 - ACTCCTGTCACTTCATCTGCGGCAAAATACAGCCCCCACCCTTACCAGAGAAAAGTGTG - 21841
21842 - TGGCATTGTAGAGAGAGGGGTTTTGCCCTCAAAGACTGTTGCTTACTTTAGTAGAATG - 21901
21902 - GGGAATGACACTGGTATCTTCCCTTAAGGGTTGTTATGGGGATGAAATGTATGTAAAGTGC - 21961
21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTCTTTGCTCGAAGTGTCTTCTGAT - 22021
22022 - GCTGCTGCTGTTGCTGCTTGTGCTTCTTCTGTGCTTACATTCTCTCTCTCACTCACTC - 22081
22082 - ACTCTGTCTCTCCTCTCCCCGCCCCACCCCTTTCTGACAAAGCCACCACCATTTTGTA - 22141
22142 - AGGAACTGTAGCTTCTCTCTGAAACTGCCGGGAAAGGAAAATCTTTTTAAATAGACAT - 22201
22202 - CACACAACCAACAGGGTCCCCTAGGTTTCAGGCGGGGAGGTGAGGTGAGTGA - 22255

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